☐ 15. Document ID: US 5712096 A

L18: Entry 15 of 19 File: USPT Jan 27, 1998

US-PAT-NO: 5712096
DOCUMENT-IDENTIFIER: US 5712096 A
TITLE: Oligoribonucleotide assays for novel antibiotics

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw. Desc | Image

☐ 16. Document ID: US 5624824 A

L18: Entry 16 of 19 File: USPT Apr 29, 1997

US-PAT-NO: 5624824
DOCUMENT-IDENTIFIER: US 5624824 A
TITLE: Targeted cleavage of RNA using eukaryotic ribonuclease P and external guide sequence

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw. Desc | Image

☐ 17. Document ID: US 5610289 A

L18: Entry 17 of 19 File: USPT Mar 11, 1997

US-PAT-NO: 5610289
DOCUMENT-IDENTIFIER: US 5610289 A
TITLE: Backbone modified oligonucleotide analogues

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw. Desc | Image

☐ 18. Document ID: US 5602240 A

L18: Entry 18 of 19 File: USPT Feb 11, 1997

US-PAT-NO: 5602240
DOCUMENT-IDENTIFIER: US 5602240 A
TITLE: Backbone modified oligonucleotide analogs

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw. Desc | Image

☐ 19. Document ID: US 5484908 A

L18: Entry 19 of 19 File: USPT Jan 16, 1996

US-PAT-NO: 5484908
DOCUMENT-IDENTIFIER: US 5484908 A
TITLE: Oligonucleotides containing 5-propynyl pyrimidines

Generate Collection

Term	Documents
(17 AND 16).USPT.	19

Display 10 Documents, starting with Document: 19

Display Format: TI Change Format

WEST

Generate Collection

Search Results - Record(s) 11 through 19 of 19 returned.

☐ 11. Document ID: US 5834253 A

L18: Entry 11 of 19 File: USPT Nov 10, 1998

US-PAT-NO: 5834253
DOCUMENT-IDENTIFIER: US 5834253 A
TITLE: Bacillus stearothermophilus DNA polymerase with proof-reading 3'-5' exonuclease activity

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw. Desc | Image

☐ 12. Document ID: US 5747298 A

L18: Entry 12 of 19 File: USPT May 5, 1998

US-PAT-NO: 5747298
DOCUMENT-IDENTIFIER: US 5747298 A
TITLE: DNA polymerase with proof-reading 3'-5' exonuclease activity Bacillus stearothermophilus

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw. Desc | Image

☐ 13. Document ID: US 5747453 A

L18: Entry 13 of 19 File: USPT May 5, 1998

US-PAT-NO: 5747453
DOCUMENT-IDENTIFIER: US 5747453 A
TITLE: Method for increasing the electrotransport flux of polypeptides

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw. Desc | Image

☐ 14. Document ID: US 5728521 A

L18: Entry 14 of 19 File: USPT Mar 17, 1998

US-PAT-NO: 5728521
DOCUMENT-IDENTIFIER: US 5728521 A
TITLE: Targeted cleavage of RNA using eukaryotic ribonuclease P and external guide sequence

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw. Desc | Image

WEST

Generate Collection

Search Results - Record(s) 1 through 10 of 19 returned.

☐ 1. Document ID: US 6117663 A

L18: Entry 1 of 19 File: USPT Sep 12, 2000

US-PAT-NO: 6117663
DOCUMENT-IDENTIFIER: US 6117663 A
TITLE: Crystal of a Ras-Sos complex

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw Desc | Image

☐ 2. Document ID: US 6117634 A

L18: Entry 2 of 19 File: USPT Sep 12, 2000

US-PAT-NO: 6117634
DOCUMENT-IDENTIFIER: US 6117634 A
TITLE: Nucleic acid sequencing and mapping

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw Desc | Image

☐ 3. Document ID: US 6077664 A

L18: Entry 3 of 19 File: USPT Jun 20, 2000

US-PAT-NO: 6077664
DOCUMENT-IDENTIFIER: US 6077664 A
TITLE: Thermophilic DNA polymerases from Thermotoga neapolitana

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw Desc | Image

☐ 4. Document ID: US 6077680 A

L18: Entry 4 of 19 File: USPT Jun 20, 2000

US-PAT-NO: 6077680
DOCUMENT-IDENTIFIER: US 6077680 A
TITLE: ShK toxin compositions and methods of use

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw Desc | Image

☐ 5. Document ID: US 6057091 A

L18: Entry 5 of 19 File: USPT May 2, 2000

US-PAT-NO: 6057091
DOCUMENT-IDENTIFIER: US 6057091 A
TITLE: Method of identifying compounds affecting hedgehog cholesterol transfer

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw Desc | Image

☐ 6. Document ID: US 6057153 A

L18: Entry 6 of 19 File: USPT May 2, 2000

US-PAT-NO: 6057153
DOCUMENT-IDENTIFIER: US 6057153 A
TITLE: Stabilized external guide sequences

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw Desc | Image

☐ 7. Document ID: US 6001645 A

L18: Entry 7 of 19 File: USPT Dec 14, 1999

US-PAT-NO: 6001645
DOCUMENT-IDENTIFIER: US 6001645 A
TITLE: Thermophilic DNA polymerases from thermotoga neapolitana

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw Desc | Image

☐ 8. Document ID: US 5965721 A

L18: Entry 8 of 19 File: USPT Oct 12, 1999

US-PAT-NO: 5965721
DOCUMENT-IDENTIFIER: US 5965721 A
TITLE: Backbone modified oligonucleotide analogues

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw Desc | Image

☐ 9. Document ID: US 5869248 A

L18: Entry 9 of 19 File: USPT Feb 9, 1999

US-PAT-NO: 5869248
DOCUMENT-IDENTIFIER: US 5869248 A
TITLE: Targeted cleavage of RNA using ribonuclease P targeting and cleavage sequences

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw Desc | Image

☐ 10. Document ID: US 5843669 A

L18: Entry 10 of 19 File: USPT Dec 1, 1998

US-PAT-NO: 5843669
DOCUMENT-IDENTIFIER: US 5843669 A
TITLE: Cleavage of nucleic acid acid using thermostable methoanococcus jannaschii FEN-1 endonucleases

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw Desc | Image

Generate Collection

Term	Documents
(17 AND 16).USPT.	19

Display 10 Documents, starting with Document: 11

Display Format: TI Change Format

WEST

Your wildcard search against 2000 terms has yielded the results below

Search for additional matches among the next 2000 terms

Generate Collection

Search Results - Record(s) 1 through 10 of 196 returned.

☐ 1. Document ID: US 6121433 A

L20: Entry 1 of 196 File: USPT Sep 19, 2000

US-PAT-NO: 6121433
DOCUMENT-IDENTIFIER: US 6121433 A
TITLE: Oligomeric compounds having nitrogen-containing linkages

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw Desc | Image

☐ 2. Document ID: US 6117663 A

L20: Entry 2 of 196 File: USPT Sep 12, 2000

US-PAT-NO: 6117663
DOCUMENT-IDENTIFIER: US 6117663 A
TITLE: Crystal of a Ras-Sos complex

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw Desc | Image

☐ 3. Document ID: US 6110745 A

L20: Entry 3 of 196 File: USPT Aug 29, 2000

US-PAT-NO: 6110745
DOCUMENT-IDENTIFIER: US 6110745 A
TITLE: Preparation of lipid-nucleic acid particles using a solvent extraction and direct hydration method

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw Desc | Image

☐ 4. Document ID: US 6110923 A

L20: Entry 4 of 196 File: USPT Aug 29, 2000

US-PAT-NO: 6110923
DOCUMENT-IDENTIFIER: US 6110923 A
TITLE: Method for treating cancer using novel substituted purinyl derivatives with immunomodulating activity

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw. Desc | Image

☐ 5. Document ID: US 6103869 A

L20: Entry 5 of 196 File: USPT Aug 15, 2000

US-PAT-NO: 6103869
DOCUMENT-IDENTIFIER: US 6103869 A
TITLE: Smad2 phosphorylation and interaction with Smad4

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw. Desc | Image

☐ 6. Document ID: US 6096875 A

L20: Entry 6 of 196 File: USPT Aug 1, 2000

US-PAT-NO: 6096875
DOCUMENT-IDENTIFIER: US 6096875 A
TITLE: Nucleotide compounds including a rigid linker

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw. Desc | Image

☐ 7. Document ID: US 6096880 A

L20: Entry 7 of 196 File: USPT Aug 1, 2000

US-PAT-NO: 6096880
DOCUMENT-IDENTIFIER: US 6096880 A
TITLE: Circular DNA vectors for synthesis of RNA and DNA

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw. Desc | Image

☐ 8. Document ID: US 6090543 A

L20: Entry 8 of 196 File: USPT Jul 18, 2000

US-PAT-NO: 6090543
DOCUMENT-IDENTIFIER: US 6090543 A
TITLE: Cleavage of nucleic acids

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw. Desc | Image

☐ 9. Document ID: US 6090606 A

L20: Entry 9 of 196 File: USPT Jul 18, 2000

US-PAT-NO: 6090606
DOCUMENT-IDENTIFIER: US 6090606 A
TITLE: Cleavage agents

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw. Desc | Image

☐ 10. Document ID: US 6087485 A

L20: Entry 10 of 196 File: USPT Jul 11, 2000

US-PAT-NO: 6087485
DOCUMENT-IDENTIFIER: US 6087485 A
TITLE: Asthma related genes

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw. Desc | Image

Generate Collection

Term	Documents
SECONDARY.USPT.	284166
SEC.USPT.	106416
STRUCTUR$	0
STRUCTUR.USPT.	100
STRUCTURA.USPT.	33
STRUCTURAAL.USPT.	2
STRUCTURABILITY.USPT.	24
STRUCTURABLE.USPT.	66
STRUCTURABLY.USPT.	10
STRUCTURADL.USPT.	1
(L18 AND SECONDARY STRUCTUR$).USPT.	196

There are more results than shown above. Click here to view the entire set.

Display [ ] Documents, starting with Document: [ ]

Display Format: [ ] Change Format

WEST

Your wildcard search against 2000 terms has yielded the results below

Search for additional matches among the next 2000 terms

Generate Collection

Search Results - Record(s) 21 through 30 of 196 returned.

☐ 21. Document ID: US 6057451 A

L20: Entry 21 of 196 File: USPT May 2, 2000

US-PAT-NO: 6057451
DOCUMENT-IDENTIFIER: US 6057451 A
TITLE: Anti-herpesvirus compounds and methods for identifying, making and using same

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw. Desc | Image

☐ 22. Document ID: US 6054442 A

L20: Entry 22 of 196 File: USPT Apr 25, 2000

US-PAT-NO: 6054442
DOCUMENT-IDENTIFIER: US 6054442 A
TITLE: Methods and compositions for modulation and inhibition of telomerase in vitro

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw. Desc | Image

☐ 23. Document ID: US 6054576 A

L20: Entry 23 of 196 File: USPT Apr 25, 2000

US-PAT-NO: 6054576
DOCUMENT-IDENTIFIER: US 6054576 A
TITLE: Deprotection of RNA

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw. Desc | Image

☐ 24. Document ID: US 6051385 A

L20: Entry 24 of 196 File: USPT Apr 18, 2000

US-PAT-NO: 6051385
DOCUMENT-IDENTIFIER: US 6051385 A
TITLE: Compositions and methods for identifying and testing therapeutics against HSV infection

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw Desc | Image

---

☐ 25. Document ID: US 6048698 A

L20: Entry 25 of 196 File: USPT Apr 11, 2000

US-PAT-NO: 6048698
DOCUMENT-IDENTIFIER: US 6048698 A
TITLE: Parallel SELEX.TM.

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw Desc | Image

---

☐ 26. Document ID: US 6048696 A

L20: Entry 26 of 196 File: USPT Apr 11, 2000

US-PAT-NO: 6048696
DOCUMENT-IDENTIFIER: US 6048696 A
TITLE: Method of identifying nucleic acid molecules

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw Desc | Image

---

☐ 27. Document ID: US 6046165 A

L20: Entry 27 of 196 File: USPT Apr 4, 2000

US-PAT-NO: 6046165
DOCUMENT-IDENTIFIER: US 6046165 A
TITLE: Compositions and methods for identifying and testing TGF-.beta. pathway agonists and antagonists

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw Desc | Image

---

☐ 28. Document ID: US 6037329 A

L20: Entry 28 of 196 File: USPT Mar 14, 2000

US-PAT-NO: 6037329
DOCUMENT-IDENTIFIER: US 6037329 A
TITLE: Compositions containing nucleic acids and ligands for therapeutic treatment

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw Desc | Image

☐ 29. Document ID: US 6037120 A

L20: Entry 29 of 196 File: USPT Mar 14, 2000

US-PAT-NO: 6037120
DOCUMENT-IDENTIFIER: US 6037120 A
TITLE: Recognition of oligonucleotides containing non-standard base pairs

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw Desc | Image

☐ 30. Document ID: US 6034218 A

L20: Entry 30 of 196 File: USPT Mar 7, 2000

US-PAT-NO: 6034218
DOCUMENT-IDENTIFIER: US 6034218 A
TITLE: Compounds and methods for immunotherapy and immunodiagnosis of prostate cancer

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw Desc | Image

Generate Collection

Term	Documents
SECONDARY.USPT.	284166
SEC.USPT.	106416
STRUCTUR$	0
STRUCTUR.USPT.	100
STRUCTURA.USPT.	33
STRUCTURAAL.USPT.	2
STRUCTURABILITY.USPT.	24
STRUCTURABLE.USPT.	66
STRUCTURABLY.USPT.	10
STRUCTURADL.USPT.	1
(L18 AND SECONDARY STRUCTUR$).USPT.	196

There are more results than shown above. Click here to view the entire set.

Display 10 Documents, starting with Document: 31

Display Format: TI Change Format

WEST

Your wildcard search against 2000 terms has yielded the results below

Search for additional matches among the next 2000 terms

Generate Collection

Search Results - Record(s) 31 through 40 of 196 returned.

☐ 31. Document ID: US 6030776 A

L20: Entry 31 of 196 File: USPT Feb 29, 2000

US-PAT-NO: 6030776
DOCUMENT-IDENTIFIER: US 6030776 A
TITLE: Parallel SELEX

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw Desc | Image

☐ 32. Document ID: US 6025140 A

L20: Entry 32 of 196 File: USPT Feb 15, 2000

US-PAT-NO: 6025140
DOCUMENT-IDENTIFIER: US 6025140 A
TITLE: Membrane-permeable constructs for transport across a lipid membrane

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw Desc | Image

☐ 33. Document ID: US 6020162 A

L20: Entry 33 of 196 File: USPT Feb 1, 2000

US-PAT-NO: 6020162
DOCUMENT-IDENTIFIER: US 6020162 A
TITLE: Crystal of a protein-ligand complex containing an N-terminal truncated eIF4E, and methods of use thereof

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw Desc | Image

☐ 34. Document ID: US 6017756 A

L20: Entry 34 of 196 File: USPT Jan 25, 2000

US-PAT-NO: 6017756
DOCUMENT-IDENTIFIER: US 6017756 A
TITLE: Method and reagent for inhibiting hepatitis B virus replication

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw Desc | Image

☐ 35. Document ID: US 6015674 A

L20: Entry 35 of 196 File: USPT Jan 18, 2000

US-PAT-NO: 6015674
DOCUMENT-IDENTIFIER: US 6015674 A
TITLE: Apparatus and method for detecting nucleic acid amplification products

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw Desc | Image

☐ 36. Document ID: US 6007987 A

L20: Entry 36 of 196 File: USPT Dec 28, 1999

US-PAT-NO: 6007987
DOCUMENT-IDENTIFIER: US 6007987 A
TITLE: Positional sequencing by hybridization

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw Desc | Image

☐ 37. Document ID: US 6004939 A

L20: Entry 37 of 196 File: USPT Dec 21, 1999

US-PAT-NO: 6004939
DOCUMENT-IDENTIFIER: US 6004939 A
TITLE: Methods for modulation and inhibition of telomerase

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw Desc | Image

☐ 38. Document ID: US 6001567 A

L20: Entry 38 of 196 File: USPT Dec 14, 1999

US-PAT-NO: 6001567
DOCUMENT-IDENTIFIER: US 6001567 A
TITLE: Detection of nucleic acid sequences by invader-directed cleavage

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw Desc | Image

☐ 39. Document ID: US 6001983 A

L20: Entry 39 of 196 File: USPT Dec 14, 1999

US-PAT-NO: 6001983
DOCUMENT-IDENTIFIER: US 6001983 A
TITLE: Oligonucleotides with non-standard bases and methods for preparing same

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw Desc | Image

☐ 40. Document ID: US 5998142 A

L20: Entry 40 of 196 File: USPT Dec 7, 1999

US-PAT-NO: 5998142
DOCUMENT-IDENTIFIER: US 5998142 A
TITLE: Systematic evolution of ligands by exponential enrichment: chemi-SELEX

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw Desc | Image

Generate Collection

Term	Documents
SECONDARY.USPT.	284166
SEC.USPT.	106416
STRUCTUR$	0
STRUCTUR.USPT.	100
STRUCTURA.USPT.	33
STRUCTURAAL.USPT.	2
STRUCTURABILITY.USPT.	24
STRUCTURABLE.USPT.	66
STRUCTURABLY.USPT.	10
STRUCTURADL.USPT.	1
(L18 AND SECONDARY STRUCTUR$).USPT.	196

There are more results than shown above. Click here to view the entire set.

Display 10 Documents, starting with Document: 41

Display Format: TI Change Format

WEST

Your wildcard search against 2000 terms has yielded the results below

Search for additional matches among the next 2000 terms

Generate Collection

Search Results - Record(s) 91 through 100 of 196 returned.

☐ 91. Document ID: US 5830653 A

L20: Entry 91 of 196 File: USPT Nov 3, 1998

US-PAT-NO: 5830653
DOCUMENT-IDENTIFIER: US 5830653 A
TITLE: Methods of using oligomers containing modified pyrimidines

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw. Desc | Image

☐ 92. Document ID: US 5827726 A

L20: Entry 92 of 196 File: USPT Oct 27, 1998

US-PAT-NO: 5827726
DOCUMENT-IDENTIFIER: US 5827726 A
TITLE: DNA coding protein kinase

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw. Desc | Image

☐ 93. Document ID: US 5824796 A

L20: Entry 93 of 196 File: USPT Oct 20, 1998

US-PAT-NO: 5824796
DOCUMENT-IDENTIFIER: US 5824796 A
TITLE: Cross-linking oligonucleotides

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw. Desc | Image

☐ 94. Document ID: US 5821356 A

L20: Entry 94 of 196 File: USPT Oct 13, 1998

US-PAT-NO: 5821356
DOCUMENT-IDENTIFIER: US 5821356 A
TITLE: Propargylethoxyamino nucleotides

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw Desc | Image

☐ 95. Document ID: US 5821234 A

L20: Entry 95 of 196 File: USPT Oct 13, 1998

US-PAT-NO: 5821234
DOCUMENT-IDENTIFIER: US 5821234 A
TITLE: Inhibition of proliferation of vascular smooth muscle cell

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw Desc | Image

☐ 96. Document ID: US 5817781 A

L20: Entry 96 of 196 File: USPT Oct 6, 1998

US-PAT-NO: 5817781
DOCUMENT-IDENTIFIER: US 5817781 A
TITLE: Modified internucleoside linkages (II)

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw Desc | Image

☐ 97. Document ID: US 5817635 A

L20: Entry 97 of 196 File: USPT Oct 6, 1998

US-PAT-NO: 5817635
DOCUMENT-IDENTIFIER: US 5817635 A
TITLE: Modified ribozymes

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw Desc | Image

☐ 98. Document ID: US 5814492 A

L20: Entry 98 of 196 File: USPT Sep 29, 1998

US-PAT-NO: 5814492
DOCUMENT-IDENTIFIER: US 5814492 A
TITLE: Probe masking method of reducing background in an amplification reaction

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw Desc | Image

☐ 99. Document ID: US 5811537 A

L20: Entry 99 of 196 File: USPT Sep 22, 1998

US-PAT-NO: 5811537
DOCUMENT-IDENTIFIER: US 5811537 A
TITLE: Antisense oligonucleotides targeted against human immunodeficiency virus

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw Desc | Image

☐ 100. Document ID: US 5811534 A

L20: Entry 100 of 196 File: USPT Sep 22, 1998

US-PAT-NO: 5811534
DOCUMENT-IDENTIFIER: US 5811534 A
TITLE: Substituted purines and oligonucleotide cross-linking

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw Desc | Image

Generate Collection

Term	Documents
SECONDARY.USPT.	284166
SEC.USPT.	106416
STRUCTUR$	0
STRUCTUR.USPT.	100
STRUCTURA.USPT.	33
STRUCTURAAL.USPT.	2
STRUCTURABILITY.USPT.	24
STRUCTURABLE.USPT.	66
STRUCTURABLY.USPT.	10
STRUCTURADL.USPT.	1
(L18 AND SECONDARY STRUCTUR$).USPT.	196

There are more results than shown above. Click here to view the entire set.

Display 10 Documents, starting with Document: 101

Display Format: TI Change Format

WEST

Your wildcard search against 2000 terms has yielded the results below

Search for additional matches among the next 2000 terms

Generate Collection

Search Results - Record(s) 141 through 150 of 196 returned.

☐ 141. Document ID: US 5672695 A

L20: Entry 141 of 196 File: USPT Sep 30, 1997

US-PAT-NO: 5672695
DOCUMENT-IDENTIFIER: US 5672695 A
TITLE: Modified ribozymes

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw. Desc | Image

☐ 142. Document ID: US 5660985 A

L20: Entry 142 of 196 File: USPT Aug 26, 1997

US-PAT-NO: 5660985
DOCUMENT-IDENTIFIER: US 5660985 A
TITLE: High affinity nucleic acid ligands containing modified nucleotides

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw. Desc | Image

☐ 143. Document ID: US 5661134 A

L20: Entry 143 of 196 File: USPT Aug 26, 1997

US-PAT-NO: 5661134
DOCUMENT-IDENTIFIER: US 5661134 A
TITLE: Oligonucleotides for modulating Ha-ras or Ki-ras having phosphorothioate linkages of high chiral purity

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw. Desc | Image

☐ 144. Document ID: US 5654284 A

L20: Entry 144 of 196 File: USPT Aug 5, 1997

US-PAT-NO: 5654284
DOCUMENT-IDENTIFIER: US 5654284 A
TITLE: Oligonucleotides for modulating RAF kinase having phosphorothioate linkages of high chiral purity

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWMC | Draw Desc | Image

☐ 145. Document ID: US 5645985 A

L20: Entry 145 of 196 File: USPT Jul 8, 1997

US-PAT-NO: 5645985
DOCUMENT-IDENTIFIER: US 5645985 A
TITLE: Enhanced triple-helix and double-helix formation with oligomers containing modified pyrimidines

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWMC | Draw Desc | Image

☐ 146. Document ID: US 5643717 A

L20: Entry 146 of 196 File: USPT Jul 1, 1997

US-PAT-NO: 5643717
DOCUMENT-IDENTIFIER: US 5643717 A
TITLE: Substrate useful for separating modified oligonucleotides

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWMC | Draw Desc | Image

☐ 147. Document ID: US 5641625 A

L20: Entry 147 of 196 File: USPT Jun 24, 1997

US-PAT-NO: 5641625
DOCUMENT-IDENTIFIER: US 5641625 A
TITLE: Cleaving double-stranded DNA with peptide nucleic acids

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWMC | Draw Desc | Image

☐ 148. Document ID: US 5639655 A

L20: Entry 148 of 196 File: USPT Jun 17, 1997

US-PAT-NO: 5639655
DOCUMENT-IDENTIFIER: US 5639655 A
TITLE: PML-RARA targeted ribozymes

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWMC | Draw Desc | Image

☐ 149. Document ID: US 5635488 A

L20: Entry 149 of 196 File: USPT Jun 3, 1997

US-PAT-NO: 5635488
DOCUMENT-IDENTIFIER: US 5635488 A
TITLE: Compounds having phosphorodithioate linkages of high chiral purity

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw Desc | Image

☐ 150. Document ID: US 5631146 A

L20: Entry 150 of 196 File: USPT May 20, 1997

US-PAT-NO: 5631146
DOCUMENT-IDENTIFIER: US 5631146 A
TITLE: DNA aptamers and catalysts that bind adenosine or adenosine-5'-phosphates and methods for isolation thereof

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw Desc | Image

Generate Collection

Term	Documents
SECONDARY.USPT.	284166
SEC.USPT.	106416
STRUCTUR$	0
STRUCTUR.USPT.	100
STRUCTURA.USPT.	33
STRUCTURAAL.USPT.	2
STRUCTURABILITY.USPT.	24
STRUCTURABLE.USPT.	66
STRUCTURABLY.USPT.	10
STRUCTURADL.USPT.	1
(L18 AND SECONDARY STRUCTUR$).USPT.	196

There are more results than shown above. Click here to view the entire set.

Display 10 Documents, starting with Document: 151

Display Format: TI Change Format

WEST

Your wildcard search against 2000 terms has yielded the results below

Search for additional matches among the next 2000 terms

Generate Collection

Search Results - Record(s) 161 through 170 of 196 returned.

☐ 161. Document ID: US 5599704 A

L20: Entry 161 of 196 File: USPT Feb 4, 1997

US-PAT-NO: 5599704
DOCUMENT-IDENTIFIER: US 5599704 A
TITLE: ErbB2/neu targeted ribozymes

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw. Desc | Image

☐ 162. Document ID: US 5599797 A

L20: Entry 162 of 196 File: USPT Feb 4, 1997

US-PAT-NO: 5599797
DOCUMENT-IDENTIFIER: US 5599797 A
TITLE: Oligonucleotides having phosphorothioate linkages of high chiral purity

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw. Desc | Image

☐ 163. Document ID: US 5595873 A

L20: Entry 163 of 196 File: USPT Jan 21, 1997

US-PAT-NO: 5595873
DOCUMENT-IDENTIFIER: US 5595873 A
TITLE: T. thermophila group I introns that cleave amide bonds

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw. Desc | Image

☐ 164. Document ID: US 5595904 A

L20: Entry 164 of 196 File: USPT Jan 21, 1997

US-PAT-NO: 5595904
DOCUMENT-IDENTIFIER: US 5595904 A
TITLE: Family of map2 protein kinases

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw Desc | Image

☐ 165. Document ID: US 5594121 A

L20: Entry 165 of 196 File: USPT Jan 14, 1997

US-PAT-NO: 5594121
DOCUMENT-IDENTIFIER: US 5594121 A
TITLE: Enhanced triple-helix and double-helix formation with oligomers containing modified purines

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw Desc | Image

☐ 166. Document ID: US 5594122 A

L20: Entry 166 of 196 File: USPT Jan 14, 1997

US-PAT-NO: 5594122
DOCUMENT-IDENTIFIER: US 5594122 A
TITLE: Antisense oligonucleotides targeted against human immunodeficiency virus

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw Desc | Image

☐ 167. Document ID: US 5594136 A

L20: Entry 167 of 196 File: USPT Jan 14, 1997

US-PAT-NO: 5594136
DOCUMENT-IDENTIFIER: US 5594136 A
TITLE: Texaphyrin solid supports and devices

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw Desc | Image

☐ 168. Document ID: US 5591600 A

L20: Entry 168 of 196 File: USPT Jan 7, 1997

US-PAT-NO: 5591600
DOCUMENT-IDENTIFIER: US 5591600 A
TITLE: Antisense inhibitors of the human immunodeficiency virus

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw Desc | Image

☐ 169. Document ID: US 5587361 A

L20: Entry 169 of 196 File: USPT Dec 24, 1996

US-PAT-NO: 5587361
DOCUMENT-IDENTIFIER: US 5587361 A
TITLE: Oligonucleotides having phosphorothioate linkages of high chiral purity

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw Desc | Image

☐ 170. Document ID: US 5580767 A

L20: Entry 170 of 196 File: USPT Dec 3, 1996

US-PAT-NO: 5580767
DOCUMENT-IDENTIFIER: US 5580767 A
TITLE: Inhibition of influenza viruses by antisense oligonucleotides

Full | Title | Citation | Front | Review | Classification | Date | Reference | Claims | KWIC | Draw Desc | Image

Generate Collection

Term	Documents
SECONDARY.USPT.	284166
SEC.USPT.	106416
STRUCTUR$	0
STRUCTUR.USPT.	100
STRUCTURA.USPT.	33
STRUCTURAAL.USPT.	2
STRUCTURABILITY.USPT.	24
STRUCTURABLE.USPT.	66
STRUCTURABLY.USPT.	10
STRUCTURADL.USPT.	1
(L18 AND SECONDARY STRUCTUR$).USPT.	196

There are more results than shown above. Click here to view the entire set.

Display 10 Documents, starting with Document: 171

Display Format: TI Change Format

L12 ANSWER 1 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1999:633269 CAPLUS
DN 131:267933
TI A method for sequencing very long DNAs with a small set of primers that can be mutated and adapted to novel sequence information
IN Brenner, Sydney
PA Lynx Therapeutics, Inc., USA
SO U.S., 28 pp., Cont.-in-part of U.S. 5,780,231.
CODEN: USXXAM
DT Patent
LA English
FAN.CNT 4

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 5962228	A	19991005	US 1997-916120	19970822 <--
	US 5763175	A	19980609	US 1995-560313	19951117 <--
	US 5780231	A	19980714	US 1996-611155	19960305 <--
	JP 11151092	A2	19990608	JP 1998-237840	19980824 <--
PRAI	US 1995-560313	19951117			
	US 1996-611155	19960305			
	US 1997-916120	19970822			

AB A novel "primer walking" method for DNA sequencing is provided that uses repeated cycles of nucleotide identification by selective extension and primer advancement along a template by template mutation. An important feature of the invention is providing a set of primers, referred to herein as "rolling primers" that contain complexity-reducing nucleotides for reducing the no. of primers required for annealing to every possible primer binding site on a sequencing template. These primers have a defined 3'-terminal region contg. complexity-reducing nucleotides (i.e. bases showing ambiguous base pairing, such as 2'-**deoxyinosine**), and a 5'-region contg. a unique sequence tag that allows it to be captured by a complementary sequence that is part of an ordered array. Another important feature of the invention is the systematic replacement of at least one of the four nucleotides in the target polynucleotide with its cognate complexity-reducing nucleotide or complement thereof. Sequencing is initiated by annealing rolling primers differing only in their terminal nucleotides to a primer binding site of a sequencing template so that only the rolling primer whose terminal nucleotide forms a perfect complement with the template leads to the formation of an extension product. After amplifying the double stranded extension product to form an amplicon, the terminal nucleotide, and hence its complement in the template, is identified by the identity of the amplicon. The primer binding site of the template of the successfully amplified polynucleotide is then mutated by, for example, **oligonucleotide**-directed mutagenesis so that a subsequent rolling primer may be selected from the set that forms a perfectly matched duplex with the mutated template at a site which is shifted towards the direction of extension by one nucleotide relative to the binding site of the previous rolling primer. The steps of selective extension, amplification and identification are then repeated. In this manner, the primers "roll" along the polynucleotide during the sequencing process, moving a base at a time along the template with each cycle. The procedure may be readily automated for large-scale sequencing projects. Use of inosine as a base in combination with other bases in the 4 3'-terminal bases allows a set of of six primers to act as the progenitors

of 200 or more primers that can be generated by mutagenesis as needed.
RE.CNT 8
RE
(1) Brenner; US 5780231 1998 CAPLUS
(2) Church; US 4942124 1990 CAPLUS
(4) Ruano; US 5427911 1995 CAPLUS
(5) Sanger; PNAS 1977, V74(12), P5463 CAPLUS
(7) Studier; US 5407799 1995 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L12 ANSWER 2 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1998:712386 CAPLUS
DN 129:311695
TI Detection and mapping of point mutations using partial digestion with nucleic acid repair enzymes
IN Chirikjian, Jack G.; Bazar, Leonard S
PA Trevigen, Inc., USA
SO PCT Int. Appl., 31 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9846793	A1	19981022	WO 1998-US6878	19980415 <--
	W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
	AU 9871030	A1	19981111	AU 1998-71030	19980415 <--
PRAI	US 1997-43184		19970416		
	WO 1998-US6878		19980415		

AB Claimed a method for detecting the presence of at least two point mutations in a target polynucleotide, as well as their relative positions and specific nucleotide positions, involving partial digestion through use of mismatch repair enzymes. First, single-stranded **oligonucleotide** probes are hybridized to targets such that double-stranded complexes are formed which contain mismatches at the sites of any point mutations. The probe strands are then partially digested with a nucleic acid repair enzyme, generating probe fragments of different sizes. Visualizing the probe fragments reveals the presence and relative positions of the point mutations. The sequence of a preferred mismatch repair enzyme, thymine DNA glycosylase, is also claimed.

L12 ANSWER 3 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1998:612101 CAPLUS
DN 129:239906
TI DNA glycosylase inhibitors and their therapeutic uses
IN Verdine, Gregory L.; Deng, Li
PA President and Fellows of Harvard College, USA
SO PCT Int. Appl., 78 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9839334	A1	19980911	WO 1998-US4604	19980309 <--

W: AU, CA, JP
RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE

AU 9867587 A1 19980922 AU 1998-67587 19980309 <--
PRAI US 1997-812653 19970307
WO 1998-US4604 19980309
OS MARPAT 129:239906
AB The present invention pertains to novel inhibitors of DNA glycosylases. The invention is based at least in part on the observation that specific substituted pyrrolidines, and analogs thereof, are capable of specifically inhibiting DNA glycosylases, e.g., as transition state analogs, and consequently are useful for modulation of DNA repair. A stereoselective, general, and practical synthetic route is developed for these inhibitors. An adenine-contg. inhibitor binds adenine glycosylase MutY specifically in a strength that surpassed the best inhibitor previously reported for any glycosylase. Such compds. can, for example, be used for treating subjects having a disorder assocd. with excessive cell proliferation, such as in the treatment of various cancers. Furthermore, these glycosylase inhibitors can be used as antibacterial, antiviral, and antifungal agents.

L12 ANSWER 4 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1998:529963 CAPLUS
TI Synthesis of DNA intrastrand crosslinks with defined structure.
AU Kowalczyk, Agnieszka; Nechev, Lubomir V.; Hodge, Richard P.; Tamura, Pamela J.; Harris, Constance M.; Harris, Thomas M.
CS Center Molecular Toxicology, Vanderbilt University, Nashville, TN, 37235, USA
SO Book of Abstracts, 216th ACS National Meeting, Boston, August 23-27 (**1998**), TOXI-097 Publisher: American Chemical Society, Washington, D. C.
CODEN: 66KYA2
DT Conference; Meeting Abstract
LA English
AB Covalent DNA lesions play important roles both in the etiol. and treatment of cancer. So far, existing strategies for synthesis of DNA intrastrand crosslinks are crosslinking agent and/or sequence specific. We are developing general protocols to prep. **oligonucleotides** contg. intrastrand crosslinks between the exocyclic amino groups of adjacent **deoxyguanosines**. **Oligonucleotides** of various length, contg. two 2-fluoro-O6-trimethylsilylethyl **deoxyinosines** were synthesized on solid supports, purified and reacted with ethylenediamine, 1,3-diaminopropane, 1,4-diaminobutane, 1,4-diamino-2R,3R-dihydroxybutane, and 1,4-diamino-2S,3S-dihydroxybutane. The latter two diamines give crosslinks which could potentially be formed by butadiene diepoxide. Reaction conditions varied with length of **oligonucleotide**. Short **oligomers** reacted well in org. media (DMSO, 55.degree.C), while longer ones required aq. conditions (borate-NaOH buffer, pH 10, 45.degree.C). The adducted **oligonucleotides** are being used for structural and biochem. studies.

L12 ANSWER 5 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1998:478973 CAPLUS
DN 129:105216
TI DNA extension and analysis with rolling primers
IN Brenner, Sydney
PA Lynx Therapeutics, Inc., USA
SO U.S., 24 pp. Cont.-in-part of U.S. Ser. No. 560,313.
CODEN: USXXAM
DT Patent
LA English

FAN.CNT 4

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 5780231	A	19980714	US 1996-611155	19960305 <--
	US 5763175	A	19980609	US 1995-560313	19951117 <--
	WO 9732999	A1	19970912	WO 1996-US18708	19961119 <--
	W: AU, CA, CN, CZ, EE, FI, HU, IS, JP, KR, LT, LV, MX, NO, NZ, PL, RU, SG, US, US				
	RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
	AU 9711619	A1	19970922	AU 1997-11619	19961119 <--
	EP 840803	A1	19980513	EP 1996-942790	19961119 <--
	R: BE, CH, DE, DK, FR, GB, IT, LI, NL, SE				
	US 5962228	A	19991005	US 1997-916120	19970822 <--
PRAI	US 1995-560313		19951117		
	US 1996-611155		19960305		
	WO 1996-US18708		19961119		

AB A novel "primer walking" method for DNA sequencing is provided that comprises repeated cycles nucleotide identification by selective extension and primer advancement along a template by template mutation. An important feature of the invention is providing a set of primers, referred to herein as "rolling primers" that contain complexity-reducing nucleotides for reducing the no. of primers required for annealing to every possible primer binding site on a sequencing template. Another important feature of the invention is the systematic replacement of at least one of the four nucleotides in the target polynucleotide with its cognate complexity-reducing nucleotide or complement thereof. Sequencing is initiated by annealing rolling primers differing only in their terminal nucleotides to a primer binding site of a sequencing template so that only the rolling primer whose terminal nucleotide forms a perfect complement with the template leads to the formation of an extension product. After amplifying the double stranded extension product to form an amplicon, the terminal nucleotide, and hence its complement in the template, is identified by the identity of the amplicon. The primer binding site of the template of the successfully amplified polynucleotide is then mutated by, for example, **oligonucleotide**-directed mutagenesis so that a subsequent rolling primer may be selected from the set that forms a perfectly matched duplex with the mutated template at a site which is shifted towards the direction of extension by one nucleotide relative to the binding site of the previous rolling primer. The steps of selective extension, amplification and identification are then repeated. In this manner, the primers "roll" along the polynucleotide during the sequencing process, moving a base at a time along the template with each cycle.

L12 ANSWER 6 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1998:221127 CAPLUS
DN 128:291114
TI **Oligonucleotide** primer probes for detection and identification of non-polio enteroviruses and serotypes
IN Kilpatrick, David
PA United States Dept. of Health and Human Services, USA; Kilpatrick, David
SO PCT Int. Appl., 48 pp.
CODEN: PIXXD2
DT Patent
LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9814611	A2	19980409	WO 1997-US17734	19971001 <--
	W: AU, CA, JP, US				
	RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				

AU 9746639 A1 19980424 AU 1997-46639 19971001 <--
EP 932702 A1 19990804 EP 1997-[redacted]433 19971001 <--
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI
PRAI US 1996-27353 19961002
WO 1997-US17734 19971001

AB This invention provides sensitive nucleic acid hybridization assay methods and kits for the detection of non-polio enterovirus and recombinant viruses (derived from poliovirus) RNA. The PCR and hybridization methods are particularly useful in detecting the presence of enterovirus nucleic acids in a biol. sample, and for ascertaining the serotype of enteroviruses present in a sample. Thus, **oligonucleotide** primer pairs are prepd. and used to detect non-polio enterovirus and to identify their serotypes. Most primers are degenerate, contain **deoxyinosine**, and detect enteroviral protein VP1. Some 48 of 49 different enterovirus serotypes can be detected using the disclosed primers. Suitable non-poliovirus-enteroviruses include coxsackie A, Coxsackie b, echoviruses, and enterovirueses 68-71. These viruses are implicated in diseases such as aseptic meningitis, enteroviral diabetes mellitus, enteroviral conjunctivitis, acute flaccid paralysis, acute benign pericarditis, exanthema, enanthema, dilated cardiomyopathy, foot-and-mouth disease, chronic fatigue syndrome, febrile illnesses, and upper respiratory tract infections.

L12 ANSWER 7 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1998:141222 CAPLUS
TI A new strategy for synthesis of DNA crosslinks.
AU Zhang, M.; Nechev, L. N.; Harris, C. M.; Harris, T. M.
CS Center Molecular Toxicology, Vanderbilt University, Nashville, TN, 37235, USA
SO Book of Abstracts, 215th ACS National Meeting, Dallas, March 29-April 2 (**1998**), MEDI-193 Publisher: American Chemical Society, Washington, D. C.
CODEN: 65QTAA
DT Conference; Meeting Abstract
LA English
AB DNA crosslinking agents play important roles both in the etiol. and treatment of cancer. We have developed new strategies to prep. **oligonucleotides** contg. crosslinks of defined structure between the exocyclic amino groups of the purine bases; these **oligonucleotides** are being used for structural and biol. studies. In our initial strategy, a crosslink was introduced after both chains, each contg. a 2-fluoro-O6-trimethylsilylethyl **deoxyinosine** residue, were synthesized and purified [Tsarouhtsis et al., J. Am. Chem. Soc. 117, 11013 (1995)]. In the alternative approach one chain (8-mer) was synthesized using a modified **deoxyguanosine** phosphoramidite contg. an FMOC-protected propylamine group at N2. After deprotection (NH4OH) and purifn. the 8-mer contg. the propylamine side chain was reacted with 8-mer contg. a 2-fluoroO6TMSE **deoxyinosine** residue (DMSO, 60.degree.C, Na2B4O7 as base) to form the crosslinked species. This approach gave a higher yield of crosslinked **oligonucleotide** than the original synthesis and should be particularly useful for the synthesis of unsym. crosslinks, intrastrand crosslinks and multiple crosslinks.

L12 ANSWER 8 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1998:89375 CAPLUS
DN 128:176921
TI High fidelity detection of nucleic acid differences by ligase detection reaction and its application to cancer mutation detection
IN Barany, Francis; Luo, Jianying; Khanna, Marilyn; Bergstrom, Donald E.
PA Cornell Research Foundation, Inc., USA; Purdue Research Foundation
SO PCT Int. Appl., 191 pp.
CODEN: PIXXD2

DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 9803673	A1	19980129	WO 1997-US12195	19970715 <--
W: AL, AM, AT, AU, AZ, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
CA 2260818	AA	19980129	CA 1997-2260818	19970715 <--
AU 9738819	A1	19980210	AU 1997-38819	19970715 <--
EP 956359	A1	19991117	EP 1997-936059	19970715 <--
R: CH, DE, GB, LI, SE				
PRAI US 1996-22535		19960719		
WO 1997-US12195		19970715		

AB Ligase detection reaction is utilized to distinguish minority template in the presence of an excess of normal template with a thermostable ligase. This process can be carried out with a thermostable ligase, a mutant thermostable ligase, or a modified **oligonucleotide** probe. Use of the mutant ligase or modified **oligonucleotide** increases the signal-to-noise ratio. This procedure is particularly useful for the detection of cancer-assocd. mutations. It has the advantage of providing a quant. measure of the amt. or ratio of minority template. K294R and K294P Thermus thermophilus DNA ligase was prepd. with recombinant E. coli.
These mutants exhibited significantly greater discrimination against single-base mismatches than did the wild-type enzyme. In a ligase detection reaction using **oligonucleotide** probes contg. 1-(2'-deoxy-.beta.-D-ribofuranosyl)pyrrole-3-carboxamide, products generated from mismatch ligation were reduced approx. 2-3-fold as compared
with regular primers.

L12 ANSWER 9 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1997:804938 CAPLUS
DN 128:102338
TI Synthesis of **oligodeoxynucleotides** containing 2-substituted guanine derivatives using 2-fluoro-2'-**deoxyinosine** as common nucleoside precursor
AU Diaz, Antonio R.; Eritja, Ramon; Garcia, Ramon Guimil
CS European Molecular Biology Laboratory, Heidelberg, D-69117, Germany
SO Nucleosides Nucleotides (**1997**), 16(10 & 11), 2035-2051
CODEN: NUNUD5; ISSN: 0732-8311
PB Marcel Dekker, Inc.
DT Journal
LA English
AB **Oligonucleotides** contg. 2-substituted guanine derivs. with double-helix stabilizing mols. such as spermine, spermidine and propylimidazole have been prepd. using protected 2-fluoro-2'-**deoxyinosine** phosphoramidite and two different protective strategies: the p-nitrophenylethyl and the t-butylphenoxyacetyl groups. Melting studies show a large increase on the melting temps. of duplexes contg. these 2-substituted guanine derivs.

L12 ANSWER 10 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1997:687648 CAPLUS
DN 127:342821
TI Substrate Specificity of Human O6-Methylguanine-DNA Methyltransferase for O6-Benzylguanine Derivatives in **Oligodeoxynucleotides**
AU Terashima, Isamu; Kawate, Hisaya; Sakumi, Kunihiko; Sekiguchi, Mutsuo;

CS Kohda, Kohfu[illegible] Faculty of P[illegible]maceutical Sciences, Nagoya Ci[illegible] University, Nagoya, 467, Japan

SO Chem. Res. Toxicol. (**1997**), 10(11), 1234-1239
CODEN: CRTOEC; ISSN: 0893-228X

PB American Chemical Society

DT Journal

LA English

AB To investigate the substrate specificity of human O6-methylguanine-DNA methyltransferase (MGMT) for O6-benzylguanine (6BG) derivs. incorporated in **oligodeoxynucleotides**, we prepd. 25-mer lengths of sequences contg. various 6BG derivs. and their related compds. and then measured the ability of these derivs. to inactivate MGMT in vitro. **Oligodeoxynucleotides** contg. a 6BG, O6-(2-fluorobenzyl)guanine (2F-6BG), O6-(3-fluorobenzyl)guanine (3F-6BG), O6-(4-fluorobenzyl)guanine (4F-6BG), O6-benzylhypoxanthine (6BH), or O6-methylguanine (6MG) were all good substrates for MGMT, and no obvious differences were obsd. among them. **Oligodeoxynucleotides** contg. N2-isobutyrated 6BG and 6MG showed only a slightly reduced capacity for inactivating MGMT compared to N2-nonmodified forms of these derivs. No obvious differences were obsd. in the corresponding double-stranded and single-stranded **oligodeoxynucleotides**. MGMT substrate specificity for the 6BG derivs. in the **oligodeoxynucleotide** was found to be quite different from that seen in our previous study. In brief, (i) 6BG, 3F-6BG, and 4F-6BG greatly inhibited human MGMT, whereas 2F-6BG, 6BH, and 6MG displayed much weaker activity; (ii) any modifications at the 2-amino group of the 6BG resulted in severe redns. in the ability to inactivate MGMT. These results obtained by the expts. using **oligodeoxynucleotides** and free bases suggest that human MGMT has low substrate specificity for 6BGs in **oligodeoxynucleotides**. Conformational changes in human MGMT which favor binding to **oligodeoxynucleotides** contg. 6BG derivs. and the subsequent transfer of their benzyl groups may account for the difference in substrate specificity between the incorporated 6BG derivs. and their free base form.

L12 ANSWER 11 OF 74 CAPLUS COPYRIGHT 2000 ACS

AN 1997:671190 CAPLUS

DN 127:304235

TI Synthesis of **Oligonucleotides** Containing the Ethylene Dibromide-Derived DNA Adducts S-[2-(N7-Guanyl)ethyl]glutathione, S-[2-(N2-Guanyl)ethyl]glutathione, and S-[2-(O6-Guanyl)ethyl]glutathione at a Single Site

AU Kim, Mi-Sook; Guengerich, F. Peter

CS Department of Biochemistry and Center in Molecular Toxicology, Vanderbilt University School of Medicine, Nashville, TN, 37232-0146, USA

SO Chem. Res. Toxicol. (**1997**), 10(10), 1133-1143
CODEN: CRTOEC; ISSN: 0893-228X

PB American Chemical Society

DT Journal

LA English

AB The carcinogen ethylene dibromide (EDB) is activated by enzymic conjugation with GSH to form S-(2-bromoethyl)GSH, which reacts with DNA via an episulfonium ion. S-[2-(N7-guanyl)ethyl]GSH has been incorporated at the G* site in d(5'-TGCTG*CAAG-3'), a site previously found to show GC to AT transitions following treatment of M13 phage with S-(2-chloroethyl)GSH, and the desired product was sepd. by HPLC. This was ligated to d(5'-GGTACCGAG-3') to yield d(5'-TGCTG*CAAGGGTACCGAG-3'). S-[2-(N2-guanyl)ethyl]GSH was incorporated into the G* site of the **oligonucleotide** in d(5'-TGCTG*CAAGGGTACCGAG-3') by reacting S-(2-aminoethyl)GSH with an **oligomer** contg. 2-fluoro-O6-[(trimethylsilyl)ethoxy]**deoxyinosine** at the target site. The 5'-(dimethoxytrityl)-N2-(phenoxyacetyl)-N-[(fluorenylmethyl)formyl] deriv.

of S-[2-(O6-deoxyguanosyl)ethyl]GSH di-Me ester was synthesized by Mitsunobu alkylation of 5'-(dimethoxytrityl)-N2-(phenoxyacetyl) **deoxyguanosine** with N-[(fluorenylmethyl)formyl]-S-(2-hydroxyethyl)GSH di-Me ester, modified to form the phosphoramidite deriv., and incorporated at the G* site of d(5'-TGCTG*CAAGGGTACCGAG-3'). The protective groups were removed with 0.10 N NaOH to give the modified **oligonucleotide** contg. S-[2-(O6-guanyl)ethyl]GSH. Although the overall yields were low, the synthesis of a single set of target site **oligonucleotides** contg. these three known guanyl adducts allows for in vitro site-specific misincorporation studies.

L12 ANSWER 12 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1997:618213 CAPLUS
DN 127:244005
TI Very large-scale simultaneous sequencing of multiple polynucleotides in a sample by capture into organized arrays with short sequence tags
IN Brenner, Sydney
PA Lynx Therapeutics, Inc., USA; Brenner, Sydney
SO PCT Int. Appl., 84 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 4

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9732999	A1	19970912	WO 1996-US18708	19961119 <--
	W: AU, CA, CN, CZ, EE, FI, HU, IS, JP, KR, LT, LV, MX, NO, NZ, PL, RU, SG, US, US				
	RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
	US 5763175	A	19980609	US 1995-560313	19951117 <--
	US 5780231	A	19980714	US 1996-611155	19960305 <--
	AU 9711619	A1	19970922	AU 1997-11619	19961119 <--
	EP 840803	A1	19980513	EP 1996-942790	19961119 <--
	R: BE, CH, DE, DK, FR, GB, IT, LI, NL, SE				
PRAI	US 1995-560313	19951117			
	US 1996-611155	19960305			
	WO 1996-US18708	19961119			

AB A method for sequencing the polynucleotides of a heterogeneous population that is suitable for automation and large-scale sequencing projects is described. Each member of the population is labeled with a unique sequence tag that is used to bind it to a complement in a spatially organized array. After a tag hybridizes with its complement and sequence information is transferred to a defined site in the array, a signal is generated, e.g. by incorporation of a label by a sequencing reaction, that gives information about the sequence that has been bound to a given site in the array. Sequences of the tagged polynucleotides are detd. by repeated cycles of amplification, information transfer, and shortening of the tagged polynucleotide by removal of the identified nucleotides. Families of rolling primers that have a repeated sequence in 5' region and variable sequences in the 3' region and that are related by progressive loss of bases at the 5'-end and addn. of bases at the 3'-end are described for use in the method. THe 3'-end of the **oligonucleotide** may include a non-specifically hybridizing base such inosine to lower the complexity of the primer family.

L12 ANSWER 13 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1997:554018 CAPLUS
DN 127:234552
TI 6-Thio-2'-**deoxyinosine**: synthesis, incorporation, and evaluation as a postsynthetically modifiable base in **oligonucleotides**

AU Coleman, Robert S.; Arthur, John C.; McCary, Jason L.
CS Dep. Chem., Ohio State Univ., Columbus, OH, 43210-1185, USA
SO Tetrahedron (**1997**), 53(32), 11191-11202
CODEN: TETRAB; ISSN: 0040-4020
PB Elsevier
DT Journal
LA English
AB The synthesis of 6-thio-2'-**deoxyinosine** (dS6I) in a form suitably protected for solid-phase **oligonucleotide** synthesis is reported. This thionucleic acid was incorporated in high yield into short **oligodeoxynucleotides**, and the thiocarbonyl group could be modified by S-alkylation with complete chemoselectivity. The quantitation of incorporation and facile post-synthetic modification was demonstrated by enzymic digestion and HPLC anal., and the effect of covalent alkylation was detd. by .DELTA.Tm measurements of the corresponding duplex **oligonucleotides** with dC as the complementary base.

L12 ANSWER 14 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1997:443862 CAPLUS
DN 127:149344
TI Synthesis of **oligodeoxynucleotides** containing 6-N-([13C]methyl)adenine and 2-N-([13C]methyl)guanine
AU Hofmann, Mechtild; Acedo, Montse; Fagan, Patricia; Wemmer, David; Eritja, Ramon; Diaz, Antonio R.
CS Eur. Mol. Biol. Lab., Heidelberg, D-69117, Germany
SO J. Chem. Soc., Perkin Trans. 1 (**1997**), (12), 1825-1828
CODEN: JCPRB4; ISSN: 0300-922X
PB Royal Society of Chemistry
DT Journal
LA English
AB **Oligonucleotides** contg. 6-N-([13C]methyl)adenine and 2-N-([13C]methyl)guanine have been prepd. for NMR studies using the deprotection step to introduce the [13C]methylamine group. For this purpose, the use of 2'-deoxy-6-O-(pentafluorophenyl)inosine and 2'-deoxy-2-fluoro-6 -O-[2-(4-nitrophenyl)-ethyl]inosine as precursors of the N-methylated nucleosides is described. Preliminary NMR characterization of the 13C-labeled **oligonucleotides** shows that the 13C chem. shift of the Me group in N-methylguanine is sensitive to duplex formation, making it a useful local probe.

L12 ANSWER 15 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1997:407967 CAPLUS
DN 127:145661
TI Studies towards the design of a modified GC base pair with stability similar to that of the AT base pair
AU Nguyen, Hong-Khanh; Asseline, Ulysse; Dupret, Daniel; Thuong, Nguyen T.
CS Centre de Biophysique Moleculaire, CNRS, Orleans, 45071, Fr.
SO Tetrahedron Lett. (**1997**), 38(23), 4083-4086
CODEN: TELEAY; ISSN: 0040-4039
PB Elsevier
DT Journal
LA English
AB Modified G*C, *GC or *G*C base pairs have been incorporated at the 3rd and 8th positions of a self-complementary decadeoxyoligonucleotide. The influence of these modifications on duplex stabilities has been studied by absorption spectroscopy. It has been found that a few of them have thermal stabilities similar to that of the AT base pair.

L12 ANSWER 16 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1997:354379 CAPLUS

DN 127:77459
TI Comparison of the base pairing properties of a series of nitroazole nucleobase analogs in the **oligodeoxyribonucleotide** sequence 5'-d(CGCXAATTYGCG)-3'
AU Bergstrom, Donald E.; Zhang, Peiming; Johnson, W. Travis
CS Dep. of Medicinal Chemistry and Molecular Pharmacology, Purdue University, West Lafayette, IN, 47907, USA
SO Nucleic Acids Res. (**1997**), 25(10), 1935-1942
CODEN: NARHAD; ISSN: 0305-1048
PB Oxford University Press
DT Journal
LA English
AB The nucleoside analogs 1-(2'-deoxy-.beta.-D-ribofuranosyl)-3-nitropyrrole, 1-(2'-deoxy-.beta.-D-ribofuranosyl)-4-nitropyrazole, 1-(2'-deoxy-.beta.-D-ribofuranosyl)-4-nitroimidazole (1), and 1-(2'-deoxy-.beta.-D-ribofuranosyl)-5-nitroindole (2) were incorporated into the **oligonucleotide** 5'-d(CGCXAATTYGCG)-3' in the fourth position from the 5'-end. Procedures for synthesis of two of the nitroazole nucleosides, 1 and 2, were developed for this study. Each of the nitroazoles was converted into a 3'-phosphoramidite for **oligonucleotide** synthesis by conventional automated protocols. Four **oligonucleotides** were synthesized for each modified nucleoside in order to obtain duplexes in which each of the four natural bases was placed opposite (position 9) the nitroazole. In order to assess the role of the nitro group on base stacking interaction, sequences were also synthesized in which the fourth base was 1-(2'-deoxy-.beta.-D-ribofuranosyl)pyrazole. Corresponding sequences contg. an abasic site, as well as sequences contg. inosine, were synthesized for comparison. Thermal melting studies yielded Tm values and thermodn. parameters. Each nucleoside analog displayed a unique pattern of base pairing preferences. The least discriminating analog was 3-nitropyrrole, for which Tm values differed by 5.degree.C and .DELTA.G25.degree.C ranged from -6.1 to -6.5 kcal/mol. 5-Nitroindole gave duplexes with significantly higher thermal stability, with Tm values varying from 35.0 to 46.5.degree.C and -.delta.G25.degree.C ranging from 7.7 to 8.5 kcal/mol. **Deoxyinosine**, a natural analog which has found extensive use as a universal nucleoside, is far less non-discriminating than any of the nitroazole derivs. Tm values ranged from 35.4.degree.C when paired with G to 62.3.degree.C when paired with C. The significance of the nitroso subsequent was detd. by comparison of the base pairing properties of a simple azole nucleoside, 1-(2'-deoxy-beta.-D-ribofuranosyl)pyrazole. The pyrazole-contg. sequences melt at 10-20.degree.C lower than the corresponding nitropyrazole-contg. sequences. On av., the pyrazole-contg. sequences were equiv. in stability (av. .DELTA.G = -4.8 kcal/mol) to the sequences contg. an abasic site (av. DELTA.G = -4.7 kcal/mol).

L12 ANSWER 17 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1997:318102 CAPLUS
DN 127:109144
TI Synthesis of stereoisomeric N6-**deoxyadenosine** adducts of syn- and anti-dihydro diol epoxides of benzo[a]pyrene and their incorporation into 18-mer DNA sequences from human Ha-ras protooncogene
AU Kroth, Heiko; Hertkorn, Norbert; Oesch, Franz; Seidel, Albrecht
CS Inst. Toxicology, Univ. Mainz, Mainz, D-55131, Germany
SO Polycyclic Aromat. Compd. (**1996**), 11(1-4), 349-356
CODEN: PARCEO; ISSN: 1040-6638
PB Gordon & Breach

DT Journal
LA English
AB **Oligonucleotide** sequences synthesized with specifically positioned and structurally defined adducts of dihydro diol epoxides (DE) of polycyclic arom. hydrocarbons like benzo[a]pyrene (B[a]P) are useful tools to study in detail the soln. structure of corresponding duplexes by NMR as well as the interaction of a single adduct with DNA polymerases. The successful incorporation of trans-N6-dA-B[a]PDE adducts derived from the syn- and anti-diastereomers of B[a]PDE into 18-mer **oligonucleotides** representing partial human Ha-ras sequences surrounding codon 61 (CAG) is reported. Key step is a nucleophilic displacement reaction of a **deoxyinosine** activated at the 6-position by a sulfonate group with a racemic amino triol providing a regio- and stereospecific synthesis of the N6-dA adducts. The amino triol precursors are prepd. by direct aminolysis of the DEs or by a stereoselective opening of the oxirane ring with NaN3 followed by redn. The fully protected diastereomeric trans-N6-dA-B[a]PDE adducts were sepd. by preparative HPLC and subsequently transformed into the corresponding phosphoramidites. The synthesis of 4 18-mers was performed on a DNA synthesizer incorporating in each sequence [d(5'-GGC-CA*G-GAG-GAG-TAC-AGC-3')] a single dA adduct (A*) at Codon 61 using std. phosphoramidite chem. After extensive purifn. of the 18-mers by reverse-phase HPLC and anal. by PAGE, the presence of the trans-N6-dA-B[a]PDE adducts in the **oligonucleotides** was confirmed by fluorescence spectroscopy.

L12 ANSWER 18 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1997:49590 CAPLUS
DN 126:186289
TI Recognition of G-C base pair by .alpha.-N7-**deoxyinosine** within the pyrimidine-purine-pyrimidine DNA triple helical motif
AU Marfurt, Judith; Hunziker, Juerg; Leumann, Christian
CS Department Chemistry Biochemistry, University Bern, Bern, CH-3012, Switz.
SO Bioorg. Med. Chem. Lett. (**1996**), 6(24), 3021-3024
CODEN: BMCLE8; ISSN: 0960-894X
PB Elsevier
DT Journal
LA English
AB The .alpha.-nucleoside 7-(2'-deoxy-.alpha.-D-ribofuranosyl)hypoxanthine, incorporated into an otherwise .beta.-configured **oligodeoxyribonucleotide** that is designed to bind to a DNA duplex in the parallel motif, recognizes selectively and efficiently a G-C base pair, presumably via monodentate .alpha.-H7.cntdot.G-C base-triple formation.

L12 ANSWER 19 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1997:14728 CAPLUS
DN 126:43598
TI **Oligonucleotide** analog probe arrays immobilized on solid substrates, target nucleic acid analogs, and probe-target improved hybridization
IN Mcgall, Glenn H.; Miyada, Charles G.; Cronin, Maureen T.; Tan, Jennifer D.; Chee, Mark S.
PA USA
SO Eur. Pat. Appl., 43 pp
CODEN: EPXXDW
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	EP 742287	A2	19961113	EP 1996-303245	19960509 <--
	EP 742287	A3	19971229		
	R: DE, FR, GB, IT, NL				

PRAI US 1995-440742 19950510
US 1996-630[illegible] 19960403
OS MARPAT 126:43598
AB **Oligonucleotide** analog arrays attached to solid substrates and methods related to the use thereof are provided. The **oligonucleotide** analogs hybridize to nucleic acids with either higher or lower specificity than corresponding unmodified **oligonucleotides**. Target nucleic acids which comprise nucleotide analogs are bound to **oligonucleotide** and **oligonucleotide** analog arrays. Examples include **oligonucleotide** probe arrays synthesized using VLSIPS (very large scale immobilized polymer synthesis), amplification of nucleic acid targets with incorporation of nucleotide analogs, and probe-target duplex thermostability anal.

L12 ANSWER 20 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1996:730537 CAPLUS
DN 126:1920
TI The tetramethylammonium chloride (TMAC) method for screening cDNA libraries with highly degenerate **oligonucleotide** probes obtained by reverse translation of amino acid sequences
AU Honore, Bent; Madsen, Peder
CS Danish Center Human Genome Research, Aarhus University, Aarhus, Den.
SO Methods Mol. Biol. (Totowa, N. J.) (1997), 69(cDNA Library Protocols), 139-146
CODEN: MMBIED; ISSN: 1064-3745
PB Humana
DT Journal
LA English
AB When using degenerate DNA probes to screen cDNA libraries by hybridization, the melting temp. of each short **oligodeoxyribonucleotide** sequence depends on the G+C content. TMAC is known to selectively bind to and stabilize A:T base pairs so that their melting temp. becomes similar to that of the G:C base pairs, thus simplifying the procedure. The TMAC technique also works with **oligonucleotides** contg. **deoxyinosine** as a neutral or slightly destabilizing base at highly ambiguous positions. Detailed protocols are provided for the TMAC method for screening cDNA libraries.

L12 ANSWER 21 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1996:718350 CAPLUS
DN 126:3771
TI Mol. screening and PCR cloning of novel endoglucanases from fungi for use as detergents, textile treatment, and paper pulp processing
IN Schuelein, Martin; Andersen, Lene Nonboe; Lassen, Soeren Flensted; Kauppinen, Markus Sakari; Lange, Lene; Nielsen, Ruby Ilum; Ihara, Michiko; Takagi, Shinobu
PA Novo Nordisk A/s, Den.
SO PCT Int. Appl., 406 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 9629397	A1	19960926	WO 1996-DK105	19960318 <--
W: AL, AM, AT, AU, AZ, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI				
RW: KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN				
CA 2214116	AA	19960926	GA 1996-2214116	19960318 <--
AU 9649394	A1	19961008	AU 1996-49394	19960318 <--

	AU 715423	B2	20000203			
	EP 815209	A1	19980107	EP 1996-305762	19960318	<--
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, PT, IE, FI					
	CN 1182451	A	19980520	CN 1996-193494	19960318	<--
	BR 9607646	A	19980616	BR 1996-7646	19960318	<--
	JP 11502701	T2	19990309	JP 1996-527993	19960318	<--
	US 6001639	A	19991214	US 1996-651136	19960521	<--
PRAI	DK 1995-272	19950317				
	DK 1995-885	19950808				
	DK 1995-886	19950808				
	DK 1995-887	19950808				
	DK 1995-888	19950808				
	DK 1996-137	19960212				
	WO 1996-DK105	19960318				

OS MARPAT 126:3771

AB Cellulolytic enzymes (endoglucanases, cellulases) were isolated from such fungi as Myceliophthora thermophila, Acremonium, Thielavia terrestris, Macrophomina phaseolina, Crinipellis scabella, Volutella colletotrichoides, and Sordaria fimicola. The cDNAs for the enzymes were isolated characterized by mol. screening and PCR cloning using degenerate, **deoxyinosine**-contg. **oligonucleotide** primers corresponding to 4 highly conserved amino acid regions found in known amino acid sequences, and DNA constructs contg. the cDNAs were used to express the enzymes in transformed Aspergillus oryzae or A. niger. The enzyme prepns. consist essentially of an enzyme having cellulolytic activity and comprise a first amino acid sequence of 14 residues having the sequence Thr-Arg-X3-X4-Asp-Cys-Cys-X8-X9-X10-Cys-X12-Trp-X14, in which X3 and X4 independently is Trp, Tyr or Phe; X8 is Arg, Lys or His; each of X9, X10, X12 and X13 is any of the 20 naturally occurring amino acid residues; and a second amino acid sequence of 5 residues having the sequence Trp-Cys-Cys-XX4-Cys in which XX4 is any of the 20 naturally occurring amino acid residues with the proviso that, in the first amino acid sequence, (i) when X12 is Ser, then X14 is not Ser, and (ii) when X12 is Gly, then X14 is not Ala. Gene fusions were also constructed between endoglucanases from Myceliophthora thermophila, Macrophomina phaseolina, and Crinipellis scabella and the linker/cellulose-binding C-terminal region of the endoglucanase from Humicola insolens. The enzymes perform excellently in detergent, laundering, textile, and papermaking pulp applications. PCR-facilitated detection of cellulolytic enzymes and their cDNA sequences are also described from 46 filamentous and monocentric fungi representing 32 genera.

L12 ANSWER 22 OF 74 CAPLUS COPYRIGHT 2000 ACS

AN 1996:672733 CAPLUS

DN 125:299781

TI Alpha-glucosidase inhibitor, composition principally comprising sugar and containing the same, sweetener, food and feed

IN Tsukada, Masayuku; Takeda, Hiroyuki; Maeda, Norio; Fukumori, Yasunori; Shiomi, Norio; Onodera, Shuichi; Fujisawa, Takuji

PA Hokuren Federation of Agricultural Cooperatives, Japan

SO Eur. Pat. Appl., 23 pp.
CODEN: EPXXDW

DT Patent

LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE	
PI	EP 738475	A1	19961023	EP 1996-102417	19960217	<--
	R: BE, DE, DK, FR, GB, IT, NL					

	JP 08289783	A2	19961105	JP 1995-119163	19950420 <--
	US 5840705	A	19981124	US 1996-[redacted]4563	19960221 <--
	AU 9650783	A1	19961031	AU 1996-50783	19960418 <--
	CA 2174602	AA	19961021	CA 1996-2174602	19960419 <--

PRAI JP 1995-119163 19950420

AB This invention relates an .alpha.-glucosidase inhibitor mildly inhibiting .alpha.-glucosidase locally present in the micro-villus of the small intestine, a compn. principally comprising sugar and contg. the inhibitor, a food, a sweetener and a feed. The inhibitor delays the digestion of starch, starch-derived **oligosaccharides** and sucrose, so that the inhibitor has an action of suppressing rapid increase in blood glucose level and an action of suppressing insulin secretion at a lower level. Thus, the inhibitor is useful for the prophylaxis of obesity and diabetes mellitus. The .alpha.-glucosidase inhibitor of the present invention is composed of nucleotide, nucleoside, or base as the structural component of nucleic acid and one or two or more digestible sugars selected from sucrose, starch and starch-derived **oligosaccharides**. The .alpha.-glucosidase inhibitor mildly inhibits the action of .alpha.-glucosidases as a digestive enzyme in the small intestine, and has the effect of suppressing rapid increase in blood glucose level and suppressing insulin secretion at a lower level. In combination with digestible sugars, the .alpha.-glucosidase inhibitor is applicable as a food, sweetener or feed.

L12 ANSWER 23 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1996:546522 CAPLUS
DN 125:214241
TI Sanger DNA sequencing by mass spectrometry using base-specific chain termination and elongation, primer modification, nested fragments, reversible immobilization, and tag-specific probes
IN Koster, Hubert
PA Sequenom, Inc., USA
SO U.S., 58 pp. Cont.-in-part of U.S. Ser. No. 1,323,abandoned.
CODEN: USXXAM
DT Patent
LA English
FAN.CNT 5

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 5547835	A	19960820	US 1994-178216	19940106 <--
	CA 2153387	AA	19940721	CA 1994-2153387	19940106 <--
	US 5605798	A	19970225	US 1995-406199	19950317 <--
	US 5691141	A	19971125	US 1995-470123	19950606 <--
	AU 9891379	A1	19990114	AU 1998-91379	19981106 <--

PRAI US 1993-1323 19930107
AU 1994-59929 19940106
US 1994-178216 19940106

AB The invention describes a new method to sequence DNA. The improvements over the existing DNA sequencing technologies are high speed, high throughput, no electrophoresis and gel reading artifacts due to the complete absence of an electrophoretic step, and no costly reagents involving various substitutions with stable isotopes. The invention utilizes the Sanger sequencing strategy and assembles the sequence information by anal. of the nested fragments obtained by base-specific chain termination via their different mol. masses using mass spectrometry, as for example, MALDI or ES mass spectrometry. A further increase in throughput can be obtained by introducing mass-modifications in the **oligonucleotide** primer, chain-terminating nucleoside triphosphates and/or in the chain-elongating nucleoside triphosphates, as well as using integrated tag sequences which allow multiplexing by hybridization of tag specific probes with mass differentiated mol. wts.

L12 ANSWER 24 OF [redacted] CAPLUS COPYRIGHT 2000 ACS
AN 1996:489726 CAPLUS
DN 125:276403
TI Post-synthetic introduction of labile functionalities onto purine residues
via 6-methylthiopurines in **oligodeoxyribonucleotides**
AU Xu, Yao-Zhong
CS Dep. Biochem. and Molecular Biol., Univ. College London, London, WC1E 6BT,
UK
SO Tetrahedron (**1996**), 52(32), 10737-10750
CODEN: TETRAB; ISSN: 0040-4020
DT Journal
LA English
AB Two methods are described for the prepn. of **oligodeoxynucleotides** contg. 6-methylthiopurine residues. 6-Methylthiopurine phosphoramidite has been prepd. and incorporated into **oligomers**. Methylation with Me iodide of 6-thiopurine (or 6-thioguanine) in **oligomers** also exclusively produces **oligomers** contg. 6-methylthiopurine (or 6-methylthioguanine). The methylthio group at defined purine residues
in the deprotected **oligomers** can be oxidized selectively and converted at the final step into various functional groups including radioactive 35S-thio group, a useful tag for crosslinking studies.

L12 ANSWER 25 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1996:448029 CAPLUS
DN 125:135674
TI G/C-modified **oligodeoxynucleotides** with selective complementarity: synthesis and hybridization properties
AU Woo, Jinsuk; Meyer, Rich B., Jr.; Gamper, Howard B.
CS Epoch Pharmaceuticals, Inc., Bothell, WA, 98021, USA
SO Nucleic Acids Res. (**1996**), 24(13), 2470-2475
CODEN: NARHAD; ISSN: 0305-1048
DT Journal
LA English
AB Modified **oligodeoxyribonucleotides** (ODNs) that have unique hybridization properties were designed and synthesized for the first time.
These ODNs, called selective binding complementary ODNs (SBC ODNs), are unable to form stable hybrids with each other, yet are able to form stable, sequence specific hybrids with complementary unmodified strands of
nucleic acid. To make SBC ODNs, **deoxyguanosine** (dG) and **deoxycytidine** (dC) were substituted with **deoxyinosine** (dI) and 3-(2'-deoxy-.beta.-D-ribofuranosyl)pyrrolo-[2,3-d]-pyrimidine-2-(3H)-one (dP), resp. The hybridization properties of several otherwise identical complementary ODNs contg. one or both of these nucleoside analogs were studied by both UV monitored thermal denaturation and non-denaturing PAGE. The data showed that while dI and dP did form base pairs with dC and dG, resp., dI did not form a stable base pair with dP. A self-complementary ODN uniformly substituted with dI and dP acquired single-stranded character and was able to strand invade the end of a duplex DNA better than an unsubstituted ODN. This observation implies that SBC ODNs should effectively hybridize to hairpins present in single-stranded DNA or RNA.

L12 ANSWER 26 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1996:217499 CAPLUS
TI Stability of **oligodeoxyribonucleotides** containing five-membered ring heterocycles.
AU Johnson, W. Travis; Zhang, Peiming; Bergstrom, Donald E.
CS Department Medicinal Chemistry and Molecular Pharmacology, Purdue University, Lafayette, IN, 47907, USA

SO Book of Abstracts, 211th ACS National Meeting, New Orleans, LA, March 24-28 (**1996**), CARB-058 Publisher: American Chemical Society, Washington, D. C.
CODEN: 62PIAJ
DT Conference; Meeting Abstract
LA English
AB The DNA double-helix is believed to be stabilized primarily by hydrogen bonding between opposing base pairs and stacking interactions among adjacent bases. We have designed and synthesized a series of .beta.-D'-deoxyribofuranosyl derivs. contg. pyrrole, pyrazole, or imidazole heterocyclic rings with polar substituents. **Oligodeoxyribonucleotides** contg. either these modifications, 2'-**deoxyinosine**, or abasic sites opposite each of the four natural deoxyribonucleosides (dA, dC, T, or dG) were also synthesized. Thermal melting profiles of the modified **oligodeoxyribonucleotides** were evaluated in order to det. the base pairing specificity of each modification. A comparison of the varying abilities of these modifications to stabilize the DNA helix is aiding in our understanding of the forces affecting helix stability. In addn., several of these nucleosides show potential as components of DNA primers and probes.

L12 ANSWER 27 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1996:181994 CAPLUS
DN 124:290179
TI Improved Strategies for Postoligomerization Synthesis of **Oligodeoxynucleotides** Bearing Structurally Defined Adducts at the N2 Position of **Deoxyguanosine**
AU DeCorte, Bart L.; Tsarouhtsis, Dimitrios; Kuchimanchi, Satyanarayan; Cooper, Monica D.; Horton, Pamela; Harris, Constance M.; Harris, Thomas M.
CS Chemistry Department, Vanderbilt University, Nashville, TN, 37235, USA
SO Chem. Res. Toxicol. (**1996**), 9(3), 630-7
CODEN: CRTOEC; ISSN: 0893-228X
DT Journal
LA English
AB Improved methodol. has been developed for prepn. of **oligodeoxynucleotides** bearing adducts on the N2 position of guanine in which the adduction reaction is carried out in homogeneous soln. rather than while the **oligonucleotide** is immobilized on a solid matrix. The methodol. utilizes a new synthon, 2-fluoro-O6-(trimethylsilylethyl)-2'-**deoxyinosine** (I). Nucleoside I is stable to the conditions of **oligodeoxyribonucleotide** synthesis, but the O6 protection is eliminated under very mild conditions following displacement of the 2-fluoro group by amine nucleophiles. **Oligonucleotides** contg. I could be removed from the solid support by treatment with 0.1 M NaOH (8 h, rt) without disruption of I. Reaction of the crude, partially deprotected **oligonucleotide** with (R)-2-amino-2-phenylethanol in homogeneous soln., followed by removal of the remaining protective groups with NH4OH (60 .degree.C, 8 h) and then 0.1% acetic acid, gave the adducted **oligonucleotide** in good purity and yield. Fully deprotected **oligodeoxyribonucleotide** contg. I could be prepd. by use of labile phenoxyacetyl-type protecting groups on the exocyclic amino groups.

L12 ANSWER 28 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1995:977032 CAPLUS
DN 124:110780
TI Interaction of **deoxyinosine** 3'-endonuclease from Escherichia coli with DNA containing **deoxyinosine**
AU Yao, Min; Kow, Yoke W.
CS Dep. Microbiol. Mol. Genet., Univ. Vermont, Burlington, VT, 05405, USA
SO J. Biol. Chem. (**1995**), 270(48), 28609-16
CODEN: JBCHA3; ISSN: 0021-9258
DT Journal

LA English
AB By using a ba[redacted]mobility shift assay, **deoxyinosine** 3'-endonuclease, an Escherichia coli enzyme which recognizes **deoxyinosine**, AP site, urea residue, and base mismatches in DNA, was shown to bind tightly to **deoxyinosine**-contg. **oligonucleotide** duplexes. Two distinct protein-DNA complexes were obsd., the faster migrating complex (complex I, Kd = 4.times.10-9 M) contained one mol. of **deoxyinosine** 3'-endonuclease, while the slower migrating complex (complex II, Kd = 4.times.10-7 M) contained two mols. of the protein bound to every mol. the duplex DNA. The endonucleolytic activity of **deoxyinosine** 3'-endonuclease paralleled the formation of the complex I. Interestingly, **deoxyinosine** 3'-endonuclease exhibited similar affinities for both the substrate and the nicked duplex product and thus remained bound to the
DNA after the cleavage reaction. The formation of a stable complex required the presence of a duplex structure 5' to the **deoxyinosine** residue. DNase I footprinting revealed that **deoxyinosine** 3'-endonuclease protected 4-5 nucleotides 5' to the **deoxyinosine**, and when complex II was formed, at least 13 nucleotides 3' to **deoxyinosine** were protected. Based on these results, a model is proposed for the interaction of **deoxyinosine** 3'-endonuclease with DNA contg. **deoxyinosine**.

L12 ANSWER 29 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1995:924794 CAPLUS
TI Non-biomimetic synthesis of site specific DNA interstrand cross-links by bifunctional pyrroles.
AU Tsarouhtsis, Dimitrios; Kuchimanchi, Satya N.; DeCorte, Bart L.; Harris, Thomas M.
CS Center Molecular Toxicology, Vanderbilt University, Nashville, TN, 37235, USA
SO Book of Abstracts, 210th ACS National Meeting, Chicago, IL, August 20-24 (**1995**), Issue Pt. 2, ORGN-180 Publisher: American Chemical Society, Washington, D. C.
CODEN: 61XGAC
DT Conference; Meeting Abstract
LA English
AB The naturally occurring retronecine alkaloids (1), after metabolic activation to the pyrrole and the synthetic pyrrole antitumor agent IPP (2) are bifunctional electrophiles which can form cross-links in DNA. These cross-links are suspected of being the basis of the carcinogenicity of 1 and the chemotherapeutic efficacy of 2. A post **oligomerization** strategy has been developed for the rational synthesis of duplex DNA bearing pyrrole crosslinks. The strategy involves reaction of the diamines derived from 1 and 2 with **oligonucleotides** contg. 2-fluoro-O6-trimethylsilylethyl- 2'-**deoxyinosine** (G*) in the **oligonucleotide** sequence 5'-AGGCG*CCT-3'. The 1:1 adduct is prepd. first followed by a second reaction with 5'-AGGCG*CCT-3'. The structures of the crosslinks were established by enzymic cleavage to yield the cross-linked bis(nucleosides) which were independently synthesized.

L12 ANSWER 30 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1995:875124 CAPLUS
DN 124:290108
TI Synthesis of **Oligonucleotides** Containing Interchain Cross-Links of Bifunctional Pyrroles
AU Tsarouhtsis, Dimitrios; Kuchimanchi, Satya; DeCorte, Bart L.; Harris, Constance M.; Harris, Thomas M.
CS Department of Chemistry, Vanderbilt University, Nashville, TN, 37235, USA
SO J. Am. Chem. Soc. (**1995**), 117(44), 11013-14

CODEN: JACSAT ISSN: 0002-7863
DT Journal
LA English
AB A method has been developed for synthesis of DNA duplexes contg. interchain cross-links between the N2 positions of **deoxyguanosines** using **oligonucleotides** contg. 2-fluoro-O6-(trimethylsilylethyl)-2'-**deoxyinosine**. The cross-links are formed by displacement of fluoride by diamines in a reversal of the normal electrophile-nucleophile relationship of mutagens with DNA. The technique has been applied to the synthesis of a DNA octamer duplex, 5'-d(AGGCGCCT)2 contg. cross-links of two agents between the 5'-(CpG) sites of the two chains. These cross-links form inefficiently and without regiochem. control by direct reaction of the bis(alkylating agents). The indirect method is significantly more efficient and controls the regiochem. of adduction.

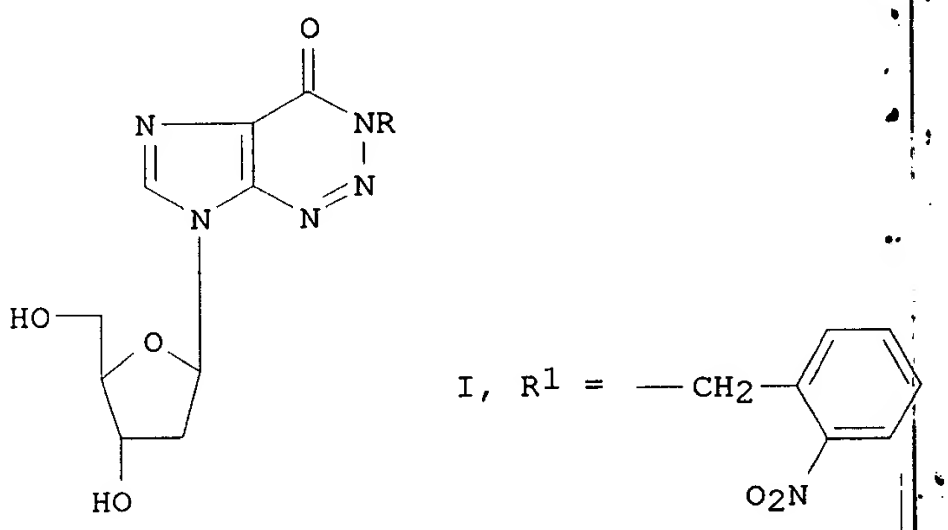
L12 ANSWER 31 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1995:810781 CAPLUS
DN 123:190516
TI **Oligonucleotide** structures with improved mismatch discrimination during hybridization and their use for analyzing the base sequence of a nucleic acid.
IN Fugono, Nobutake; Kurusu, Yasurou; Terasawa, Masato; Yukawa, Hideaki
PA Mitsubishi Chemical Corp., Japan
SO Eur. Pat. Appl., 23 pp.
CODEN: EPXXDW
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	EP 668361	A1	19950823	EP 1995-102435	19950221 <--
	EP 668361	B1	20000419		
	R: BE, DE, FR, GB, IT, NL				
	JP 08070900	A2	19960319	JP 1995-24410	19950213 <--
	US 5738993	A	19980414	US 1996-662963	19960613 <--
PRAI	JP 1994-24168		19940222		
	JP 1994-147291		19940629		
	US 1995-392147		19950222		

AB A novel **oligonucleotide** structure is described which allows high-sensitivity hybridization and can clearly discriminate a hybrid having a mismatched terminus from a completely complementary hybrid, and thus can be used in a method for analyzing the base sequence of a nucleic acid. The **oligonucleotide** comprises a specific region and 1 or 2 nonspecific regions which are bound to at least one of the 2 termini of the specific region, such that the specific region has a specific base sequence which is substantially complementary to a target sequence of a sample nucleic acid with which the **oligonucleotide** is to be hybridized, and the nonspecific region is composed of at least one nucleotide having another base capable of forming a base pair with each of bases constituting a common nucleic acid. A specific example of such "another" base is hypoxanthine or the deoxyribonucleotide **deoxyinosine**, which can form a base pair with any nucleotide. When the **oligonucleotide** is used as a probe for hybridization, it may be used in a form immobilized on an insol. carrier. The amt. of hybridization varies depending on the sequence of the specific region, but increases in any sequence by introducing inosine (nonspecific region) in both the 3' and 5' termini. The ability to identify a mismatch (discrimination value) was excellent with an **oligonucleotide** having inosine in both termini. A surface-active agent (sodium N-lauroylsarcosinate) improves the sensitivity of the hybridization.

L12 ANSWER 32 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1995:806967 CAPLUS

DN 124:202868
TI Synthesis and [redacted]iophysical and Biological Prop[redacted]ies of **Oligonucleotides** Containing 2-Aza-2'-**Deoxyinosine**
AU Acedo, Montse; De Clercq, Erik; Eritja, Ramon
CS Centro de Investigacion y Desarrollo, C. S. I. C., Barcelona, 08034, Spain
SO J. Org. Chem. (**1995**), 60(20), 6262-9
CODEN: JOCEAH; ISSN: 0022-3263
DT Journal
LA English
GI



I, R^1 = —CH_2—

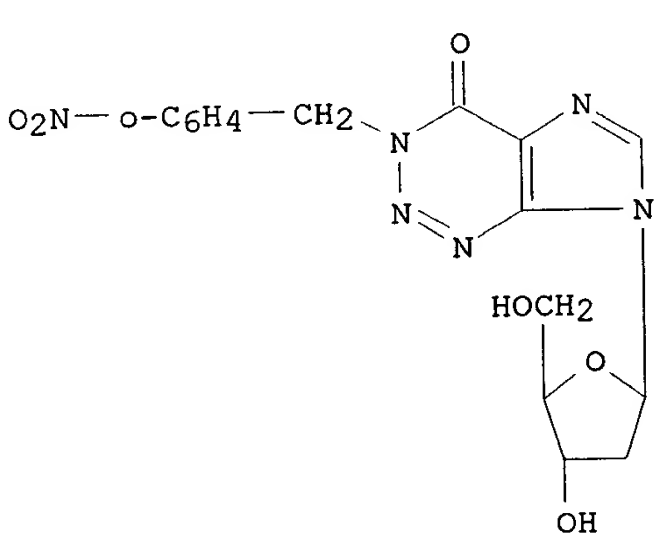
AB 2-Aza-2'-**deoxyinosines**, e.g. I (R = H, R1), were prepd. and incorporated into **oligodeoxyribonucleotide** duplexes. Protection of the 2-azahypoxanthine moiety with the photolabile 2-nitrobenzyl group enabled us to obtain the phosphoramidite deriv. and **oligodeoxyribonucleotides** contg. protected 2-aza-2'-**deoxyinosine**. After purifn., photolysis of the **oligonucleotides** contg. the protected analog provided the desired **oligonucleotides** in good yields. Melting curves of duplexes contg. 2-azahypoxanthine paired with the four natural bases at pH 6 and pH 8 proved that 2-azahypoxanthine base pairs were less stable than perfectly matched duplexes but showed little variation among different bases. Compds. I showed no significant antiviral and cytotoxicity activities.

L12 ANSWER 33 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1995:703893 CAPLUS
DN 123:340726
TI **Oligodeoxynucleotides** embodying the ambiguous base Z, 5-aminoimidazole-4-carboxamide
AU Pochet, Sylvie; Dugue, Laurence
CS Departement BGM, Institut Pasteur, Paris, 75754, Fr.
SO Nucleosides Nucleotides (**1995**), 14(6), 1195-210
CODEN: NUNUD5; ISSN: 0732-8311
DT Journal
LA English
OS CASREACT 123:340726
AB **Oligomers** d(ZAC) and d(CACZAC) (dZ = 5-amino-1-(2-deoxy-.beta.-D-ribofuranosyl)imidazole-4-carboxamide) were synthesized in soln. using the phosphotriester methodol. Usual acyl groups were used for the canonical bases. For the exocyclic amino function of Z residue, the hydrogenolyzable benzyloxycarbonyl group was introduced.

L12 ANSWER 34 OF 74 CAPLUS COPYRIGHT 2000 ACS

AN 1995:631157 CAPLUS
DN 123:131985
TI Structure-activity study of **oligodeoxynucleotides** which inhibit thrombin
AU Krawczyk, Steven H.; Bischofberger, Norbert; Griffin, Linda C.; Law, Veronica S.; Shea, REgan G.; Swaminathan, S.
CS Gilead Sciences, Foster City, CA, 94404, USA
SO Nucleosides Nucleotides (**1995**), 14(3-5), 1109-16
CODEN: NUNUD5; ISSN: 0732-8311
DT Journal
LA English
AB The 15-mer **oligodeoxynucleotide** GGTTGGTGTGGTTGG is a potent inhibitor of thrombin and it forms a stable, highly compact structure in soln. Deletions and substitutions by abasic residues, 2'-**deoxyinosine**, 7-deaza-2'-**deoxyguanosine** and 8-methyl-2'-**deoxyguanosine** show that the structural features of the **oligodeoxynucleotide** are important for its biol. activity.

L12 ANSWER 35 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1995:631091 CAPLUS
DN 124:202865
TI Preparation of **oligonucleotides** containing non-natural base analogs
AU Eritja, Ramon; Acedo, Montse; Avino, Anna; Fabrega, Carme
CS Dep. of Molecular Genetics, CID-CSIC, Barcelona, 08034, Spain
SO Nucleosides Nucleotides (**1995**), 14(3-5), 821-4
CODEN: NUNUD5; ISSN: 0732-8311
DT Journal
LA English
GI

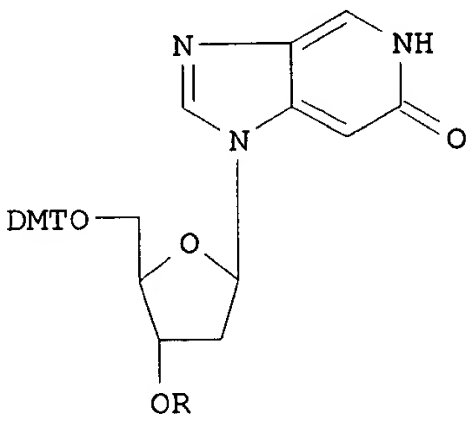


I

AB The prepn. of 2-aza-2'-**deoxyinosine** carrying a photolabile protecting group (I) is described. I is useful in prepg. **oligonucleotides** contg. 2-azahypoxanthine. The synthesis of **oligonucleotides** contg. 2-fluorohypoxanthine and the mutagenic bases O4-benzyl- and O4-butylthymine is also described.

L12 ANSWER 36 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1995:631087 CAPLUS
DN 123:314341
TI Chemical and enzymic synthesis of 2'-deoxy-iso-inosine and its incorporation into DNA
AU Beaussire, Jean-Jacques; Pochet, Sylvie
CS Dep. BGM, Inst. Pasteur, Paris, 75724, Fr.
SO Nucleosides Nucleotides (**1995**), 14(3-5), 805-8
CODEN: NUNUD5; ISSN: 0732-8311
DT Journal

LA English
GI



I

AB Two procedures for the prepn. of 2'-deoxy-iso-inosine I (R = H) (II) are presented. Synthesis of 3'-phosphoramidite and 3'-phosphonate I [R = P(OCH2CH2CN)N(CHMe2)2, HP(O)OEt3NH] are described, as well as an **oligodeoxyribonucleotide** contg. iso-II.

L12 ANSWER 37 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1995:613672 CAPLUS
DN 123:189453
TI **Deoxyinosine**-containing primers for solid-phase, automated DNA sequencing
AU Mollet, Christophe; Drancourt, Michel; Raoult, Didier
CS Faculte de Medecine, Unite des Rickettsies, Marseille, 13385, Fr.
SO Methods Mol. Cell. Biol. (**1995**), Volume Date 1994, 5(2), 125-7
CODEN: MMCBEV; ISSN: 0898-7750
DT Journal
LA English
AB An original strategy was developed to perform solid-phase sequencing of an amplified bacterial gene. Design of sequencing primers was based on the consensus sequences of related genes in different bacterial species. Ambiguities were resolved using inosine-contg. primers instead of degenerate primers as previously used. The data show that such **deoxyinosine**-contg. primers can be used for direct, solid-phase automated sequencing, for up to 3 **deoxyinosine** residues for a 20-mer primer.

L12 ANSWER 38 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1995:603614 CAPLUS
DN 123:76185
TI 1H and 31P resonance assignments and secondary structure of hairpin conformer of IA mismatched **oligonucleotide** d-GGTACIAGTACC
AU Chary, Kandala V. R.; Rastogi, Vinit K.; Govil, Girjesh; Howard, Frank B.; Miles, H. Todd
CS Chem. Phys. Group, Tata Inst. Fundamental Res., Bombay, 400 005, India
SO Proc. - Indian Acad. Sci., Chem. Sci. (**1994**), 106(7), 1491-504
CODEN: PIAADM; ISSN: 0253-4134
DT Journal
LA English
AB Almost complete 1H and 31P resonance assignments of two coexisting conformers (duplex and an hairpin) of d-GGTACIAGTACC at 1.25 mM concn. and 305 K have been achieved. The results demonstrate that the hairpin conformer has a structure with two purines I6 and A7 forming a two-base loop on a B-DNA stem. Stacking is continued on the 5'-side of the loop, with the I6 stacked upon C5. The base A7, on the 3'-side of the loop stacks partially with I6. The glycosidic angle for G8 is in the anti

domain and it maintains normal Watson-Crick base-pairing with the opposite
C5.

L12 ANSWER 39 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1995:481729 CAPLUS
DN 122:308473
TI Solution Conformation of the N-(Deoxyguanosin-8-yl)aminofluorene Adduct opposite **Deoxyinosine** and **Deoxyguanosine** in DNA by NMR and Computational Characterization
AU Abuaf, Perlette; Hingerty, Brian E.; Broyde, Suse; Grunberger, Dezider
CS College of Physicians and Surgeons, Columbia University, New York, NY, 10032, USA
SO Chem. Res. Toxicol. (**1995**), 8(3), 369-78
CODEN: CRTOEC; ISSN: 0893-228X
DT Journal
LA English
AB Two-dimensional proton NMR and energy minimization computations have been employed to characterize the conformations of the N-(deoxyguanosin-8-yl)aminofluorene adduct [(AF)G] positioned opposite **deoxyguanosine** in one, and opposite **deoxyinosine** in another DNA undecamer duplex in aq. soln. The two **oligomer** duplexes used in this study are d[C1-C2-A3-T4-C5-(AF)G6-C7-T8-A9-C10-C11].cntdot.[G12-G13-T14-A15-G16-X17-G18-A19-T20-G21-G22], where X17 was **deoxyinosine** in one duplex and **deoxyguanosine** in another. The exchangeable and nonexchangeable protons of the DNA are well resolved and narrow in the NMR
spectra of the duplexes, and the base and sugar nucleic acid protons were assigned by NOESY and COSY data sets. All nine of the nonexchangeable aminofluorene ring protons were also assigned for the duplex that has **deoxyinosine** across from the modification site, and the (AF)G.cntdot.I structure was employed to model the (AF)G.cntdot.G one. The NOE distance restraints establish that the glycosidic torsion angle at
(AF)G6 is syn. All other glycosidic torsion angles are anti, Watson-Crick
type A.cntdot.T and G.cntdot.C base pairing is intact throughout the duplex except at the site of modification, and the helix maintains an overall B-DNA conformation. The syn orientation at the (AF)G6 places the aminofluorene ring in the B-DNA minor groove in a conformation similar to that found previously when the (AF)G was positioned opposite **deoxyadenosine** [D. Norman et al. (1989)].

L12 ANSWER 40 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1995:320560 CAPLUS
DN 122:207983
TI Cloning and expression of human neutrophil lipocalin cDNA derived from bone marrow and ovarian cancer cells
AU Bartsch, Stefan; Tschesche, Harald
CS Department of Biochemistry, University of Bielefeld, Universitaetsstrasse 25, Bielefeld, 33615, Germany
SO FEBS Lett. (**1995**), 357(3), 255-9
CODEN: FEBLAL; ISSN: 0014-5793
DT Journal
LA English
AB Human neutrophil lipocalin (HNL) cDNA was amplified by PCR technol. in combination with **deoxyinosine**-contg. **oligonucleotides** for cloning, sequencing, and prodn. of the recombinant protein in Escherichia coli. The primers were targeted to the corresponding DNA backtranslate of the mature protein resulting in a PCR amplified 534-bp cDNA from different reverse transcripts of ovarian cancer cell line and bone marrow cell mRNAs. Sequence anal. revealed that 2 different cDNAs from ovarian cancer and bone marrow cells could be obtained. Cloning and expression of HNL cDNAs were performed in E. coli strain HMS 174 [DE3] using the pET system yielding 2 recombinant proteins with a mol. wt. of

kDa which is consistent with an 178-amino-acid sequence of the mature HNL protein. N-terminal amino acid sequence analysis of the expression products showed an identical polypeptide sequence missing the E. coli processed starting methionine.

L12 ANSWER 41 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1995:315534 CAPLUS
DN 122:133688
TI Preparation of boronated purine and pyrimidine bases, nucleosides, phosphate esters, and **oligomers** as drugs.
IN Spielvogel, Bernard F.; Sood, Anup; Hall, Iris H.; Shaw, Barbara Ramsay; Tomasz, Jeno
PA Boron Biologicals, Inc., USA; Duke University
SO PCT Int. Appl., 55 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 3

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 9401413	A1	19940120	WO 1993-US6230	19930629 <--
W: AU, CA, JP				
RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
US 5362732	A	19941108	US 1992-909950	19920707 <--
AU 9346585	A1	19940131	AU 1993-46585	19930629 <--
EP 649411	A1	19950426	EP 1993-916875	19930629 <--
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE				

PRAI US 1992-909950 19920707
US 1989-453311 19891220
WO 1993-US6230 19930629
OS CASREACT 122:133688; MARPAT 122:133688
AB Boronated purine and pyrimidine bases and boronated nucleosides, as well as phosphate esters and **oligomers** thereof, in which the boron-contg. substitutent is BH2CN, BH3, BF3, BH2CO2R, BH2CONHR (R = H, alkyl), were prepd. The compds. are boronated at a ring nitrogen of the purine or pyrimidine base, or at a 2', 3', or 5' amino substituent of the nucleoside sugar. Thus, 2'-**deoxyadenosine** and triphenylphosphine cyanoborane were stirred in DMF to give 11.3% N7-cyanoborano-2'-**deoxyadenosine** and 34.3% N1-cyanoborano-2'-**deoxyadenosine**. Adenine-N1-cyanoborane showed ED50 = 1.29 .mu.g/mL against murine L-1210. Title compds. also showed antiinflammatory, analgesic, and hypolipidemic activity. 2'-**Deoxyguanosine**-N7-cyanoborane-5'-triphosphate was used to prep. boronated **oligonucleotide** via PCR.

L12 ANSWER 42 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1995:255610 CAPLUS
DN 122:96505
TI Preparation of boronated compounds and antihyperlipidemic, anti-inflammatory, and analgesic activities thereof
IN Spielvogel, Bernard F.; Sood, Anup; Hall, Iris H.; Shaw, Barbara R.; Tomasz, Jeno
PA University of North Carolina at Chapel Hill, USA; Boron Biologicals; Duke University
SO U.S., 12 pp. Cont.-in-part of U.S. 5,130,302.
CODEN: USXXAM
DT Patent
LA English
FAN.CNT 3

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI US 5362732	A	19941108	US 1992-909950	19920707 <--
US 5130302	A	19920714	US 1989-453311	19891220 <--
CA 2071936	AA	19910621	CA 1990-2071936	19901217 <--

	AT 159027	E	19971015	AT 1991-905077	19901217 <--
	WO 9401413	A1	19940120	WO 1993-US6230	19930629 <--
	W: AU, CA, JP				
	RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
	AU 9346585	A1	19940131	AU 1993-46585	19930629 <--
	EP 649411	A1	19950426	EP 1993-916875	19930629 <--
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE				
	US 5659027	A	19970819	US 1994-334745	19941104 <--
PRAI	US 1989-453311	19891220			
	US 1992-909950	19920707			
	WO 1993-US6230	19930629			

AB A novel class of pharmaceutically active boronated compds. are provided. The boronated compds. include boronated purine and pyrimidine bases and boronated nucleosides, as well as phosphate esters and **oligomers** thereof. The compds. are boronated at the ring nitrogen of the purine or pyrimidine base, or at a 2'-, 3'- or 5'-amino substituent of the nucleoside sugar. For example, adenine-N1-cyanoborane was prepd. and tested for its biol. activities, i.e. cytotoxic, antitumor, anti-inflammatory, hypolipidemic, and analgesic activity.

L12 ANSWER 43 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1995:187740 CAPLUS
DN 122:127285
TI **Deoxyinosine** 3' endonuclease, a novel **deoxyinosine** -specific endonuclease from Escherichia coli
AU Yao, Min; Hatahet, Zafer; Melamede, Robert J.; Kow, Yoke W.
CS Markey Center Molecular Genetics, University Vermont, Burlington, VT, 05405, USA
SO Ann. N. Y. Acad. Sci. (**1994**), 726(DNA DAMAGE, EFFECTS ON DNA STRUCTURE AND PROTEIN RECOGNITION), 315-16
CODEN: ANYAA9; ISSN: 0077-8923
DT Journal
LA English
AB **Deoxyinosine** 3' endonuclease (D3'E) was purified from E. coli and migrated as a 26-kDa polypeptide and required Mg2+ for activity. D3'E was active on **oligonucleotides** contg. I/T, I/C, I/A, and I/G pairs. D3'E cut the 2nd phosphodiester bond 3' to **deoxyinosine** for all **deoxyinosine** pairs and **deoxyinosine**-contg. single-stranded DNAs, as well as DNA contg. the AP site. D3'E creates a nick with 3' hydroxyl group since the product of D3'E is a substrate for nick translation.

L12 ANSWER 44 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1995:20199 CAPLUS
DN 122:2065
TI Use of **deoxyinosine**-containing primers vs degenerate primers for polymerase chain reaction based on ambiguous sequence information
AU Rossolini, Gian Maria; Cresti, Stefania; Ingianni, Angela; Cattani, Paola; Riccio, Maria Letizia; Satta, Giuseppe
CS Dip. Biol. Mol., Univ. Siena, Siena, 53100, Italy
SO Mol. Cell. Probes (**1994**), 8(2), 91-8
CODEN: MCPRE6; ISSN: 0890-8508
DT Journal
LA English
AB The performance of **oligonucleotide** primers contg. **deoxyinosine** (dI) at all ambiguous positions for polymerase chain reaction, based on ambiguous sequence information derived either from compilations of consensus nucleotide sequences or from amino acid sequences, has been evaluated in two model systems represented resp. by amplification of conserved genomic regions from different types of human papillomavirus and by amplification of a region of the human lysozyme cDNA

on the basis of the protein amino acid sequence. In both instances the dI-contg. primers obtained the expected amplification products. When using short primers or primers with very high dI contents, however, peculiar reaction conditions had to be adopted to obtain successful amplification and, in the latter case, performance remained suboptimal. Comparison of results with those obtained using corresponding degenerate primers showed that the use of dI-contg. primers can be advantageous in terms of both specificity and yield of the amplification product. Sequence anal. of amplification products showed that dG residues are always found at positions corresponding to the dI residues of the primers.

L12 ANSWER 45 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1995:17946 CAPLUS
DN 122:2059
TI Application of PCR with **oligonucleotide** primers containing **deoxyinosine** for gene detection, isolation and sequencing
AU Palva, Airi; Vidgren, Gabriele; Paulin, Lars
CS Food Res. Inst., Agric. Res. Cent. Finland, Jokioinen, SF-31600, Finland
SO J. Microbiol. Methods (**1994**), 19(4), 315-21
CODEN: JMIMDQ; ISSN: 0167-7012
DT Journal
LA English
AB We have used the polymerase chain reaction (PCR) in combination with inosine contg. primers to detect, isolate and sequence the S-layer protein from Lactobacillus brevis without previous knowledge of its DNA sequence. Degeneracy of the **oligonucleotide** primers, designed from the N-terminal sequences of the intact protein and its internal peptides, were lowered significantly by introducing **deoxyinosine** to the ambiguous codon positions. This enabled the use of these primers throughout the entire gene characterization. This approach was the method of choice, since conventional techniques to isolate this gene failed due to the instability of the gene in Escherichia coli and Bacillus subtilis. The combination of methods described here is widely applicable for detection, isolation and sequencing of any gene of interest.

L12 ANSWER 46 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1995:12962 CAPLUS
DN 122:97669
TI Cloning and sequencing analysis of homeobox transcription factor cDNAs with an inosine-containing probe
AU Gorski, David H.; LePage, David F.; Walsh, Kenneth
CS Sch. Med., Case Western Res. Univ., Cleveland, OH, USA
SO BioTechniques (**1994**), 16(5), 856,858,860-2,865
CODEN: BTNQDO; ISSN: 0736-6205
DT Journal
LA English
AB Much effort has been directed toward the isolation and characterization of homeobox cDNAs form numerous cell types because they encode transcription factors important to many cellular processes, including pattern formation in the embryo, cell growth and cell differentiation. Many novel homeobox cDNAs have been isolated by screening libraries by hybridization with degenerate **oligonucleotides** designed from conserved amino acid sequences in the third helix of the homeodomain. However, the degeneracy of the genetic code necessitates that these **oligonucleotides** be highly degenerate, often precluding their use as sequencing primers to rapidly det. clone identity. Here we describe a screening protocol for homeobox cDNAs that utilizes a short **oligonucleotide** probe with inosine residues incorporated at positions of max. codon degeneracy. This probe specifically hybridizes to many classes of homeobox transcription

factor cDNAs, but its primary advantage is that it also serves as an effective sequencing primer, which allows the investigator to rapidly det.
whether the clones encode a protein of interest. In a screen of 500,000 plaques of a rat aorta cDNA library by this method, we identified 13 pos. plaques of which 12 were found to contain homeobox cDNAs representing 5 distinct genes, and, using this probe, it was possible to obtain initial high-quality sequence information from every clone isolated that contained
a homeodomain.

L12 ANSWER 47 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1995:4161 CAPLUS
DN 122:126439
TI Investigations of **oligodeoxyinosine** for triple helix formation
AU Hogeland, Jane S.; Weller, Dwight D.
CS Dep. Chem., Oregon State Univ., Corvallis, OR, 97331, USA
SO Antisense Res. Dev. (**1993**), 3(3), 285-90
CODEN: AREDEI; ISSN: 1050-5261
DT Journal
LA English
AB The ability of a 17-mer of **deoxyinosine** to form a triple helix with a (dT)17(dA)17 segment of a 29-mer Watson-Crick duplex was investigated. Under conditions amenable to triple helix formation, (dT)17
showed evidence of complex formation as evidenced by UV melting curves and
gel mobility shift assays whereas (dT)17 did not.

L12 ANSWER 48 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1994:658245 CAPLUS
DN 121:258245
TI DNA sequencing by mass spectrometry
IN Koester, Hubert
PA USA
SO PCT Int. Appl., 94 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 5

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9416101	A2	19940721	WO 1994-US193	19940106 <--
	WO 9416101	A3	19941124		
	W: AU, CA, CN, JP, RU				
	RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
	CA 2153387	AA	19940721	CA 1994-2153387	19940106 <--
	AU 9459929	A1	19940815	AU 1994-59929	19940106 <--
	AU 694940	B2	19980806		
	EP 679196	A1	19951102	EP 1994-906047	19940106 <--
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE				
	JP 08509857	T2	19961022	JP 1994-516209	19940106 <--
	AU 9891379	A1	19990114	AU 1998-91379	19981106 <--
PRAI	US 1993-1323		19930107		
	AU 1994-59929		19940106		
	WO 1994-US193		19940106		

AB The invention describes a new method to sequence DNA. The improvements over the existing DNA sequencing technologies are high speed, high throughput, no electrophoresis and gel reading artifacts due to the complete absence of an electrophoretic step, and no costly reagents involving various substitutions with stable isotopes. The invention utilizes the Sanger sequencing strategy and assembles the sequence information by anal. of the nested fragments obtained by base-specific chain termination via their different mol. masses using mass spectrometry,

as for example, MALDI or ES mass spectrometry. A further increase in throughput can be obtained by introducing mass modifications in the **oligonucleotide** primer, chain-terminating nucleoside triphosphates and/or in the chain-elongating nucleoside triphosphates, as well as using integrated tag sequences which allow multiplexing by hybridization of tag specific probes with mass-differentiated mol. wts.

L12 ANSWER 49 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1994:452899 CAPLUS
DN 121:52899
TI .alpha.-**Deoxyadenosine**, a Major Anoxic Radiolysis Product of Adenine in DNA, Is a Substrate for Escherichia coli Endonuclease IV
AU Ide, Hiroshi; Tedzuka, Kei; Shimzu, Hironori; Kimura, Yoshiharu; Purmal, Andrei A.; Wallace, S. S.; Kow, Y. W.
CS Department of Polymer Science and Engineering, Kyoto Institute of Technology, Kyoto, 606, Japan
SO Biochemistry (**1994**), 33(25), 7842-7
CODEN: BICHAW; ISSN: 0006-2960
DT Journal
LA English
AB **Oligonucleotides** contg. a unique .alpha.-**deoxyadenosine** or THF (a model abasic site) were synthesized using phosphoramidite chem. Repair enzymes from Escherichia coli, including endonucleases III, IV, and VIII, exonuclease III, formamidopyrimidine N-glycosylase, and **deoxyinosine** 3'-endonuclease, as well as UV dimer N-glycosylases from T4 (den V) and Micrococcus luteus, were examd. for their ability to recognize .alpha.-**deoxyadenosine** and THF. In agreement with prior studies, a tetrahydrofuran-contg. **oligonucleotide** was a substrate for endonuclease IV and exonuclease III, but not for the other repair enzymes. However, an **oligonucleotide** contg. .alpha.-deoxyadenine was a substrate only for endonuclease IV. Competitive inhibition studies with both substrates confirmed that the activity recognizing .alpha.-deoxyadenine was endonuclease IV and not a possible contaminant in the endonuclease IV prepn. Using E. coli exts., the activity that recognized .alpha.-deoxyadenine was dependent on nfo, the structural gene of endonuclease IV, further substantiating that endonuclease IV is the enzyme that recognized .alpha.-deoxyadenine. Kinetic measurements indicated that .alpha.-**deoxyadenosine** was as good a substrate for endonuclease IV as tetrahydrofuran; the Km and Vmax values for both substrates were similar. Using substrates that were labeled at either the 3'- or 5'-terminus, endonuclease IV was shown to hydrolyze the phosphodiester bond 5' to either .alpha.-**deoxyadenosine** or THF, leaving the lesion, .alpha.-**deoxyadenosine** or THF, on the 5'-terminus of the nicked site. The ability of endonuclease IV to recognize .alpha.-**deoxyadenosine** suggests that endonuclease IV is able to recognize a new class of DNA base lesions that is not recognized by other DNA N-glycosylases and AP endonucleases.

L12 ANSWER 50 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1994:429736 CAPLUS
DN 121:29736
TI Substrate specificity of Fpg protein. Recognition and cleavage of oxidatively damaged DNA
AU Tchou, Julia; Bodepudi, Veeraiah; Shibutani, Shinya; Antoshechkin, Igor; Miller, Jeffrey; Grollman, Arthur P.; Johnson, Francis
CS Dep. Pharmacol. Sci., State Univ. New York, Stony Brook, NY, 11794-8654, USA
SO J. Biol. Chem. (**1994**), 269(21), 15318-24
CODEN: JBCHA3; ISSN: 0021-9258
DT Journal
LA English
AB Formamidopyrimidine-DNA glycosylase (Fpg protein) (I) of Escherichia coli,

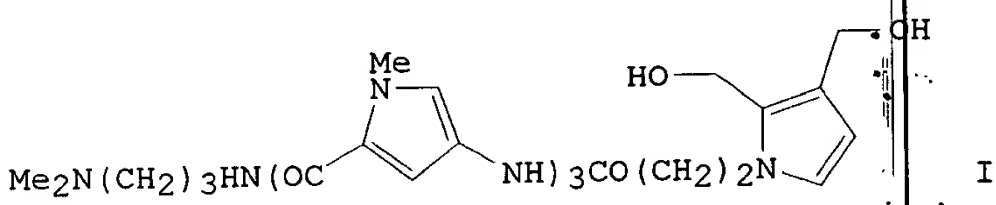
also known as 8-oxoguanine-DNA glycosylase, has N-glycosylase and apurinic/apyrimidinic lyase activities. It recognizes oxidative DNA damage by efficiently removing formamidopyridine lesions and 8-oxoguanine residues from DNA. Defined **oligodeoxynucleotides** contg. various 8-oxopurines were used to examine the substrate specificity of I and to establish the role of functional groups in DNA on damage recognition and catalysis. Binding affinities of I were established for duplex **oligodeoxynucleotides** contg. 8-oxo-2'-deoxyguanine, 8-oxo-2'-deoxyadenine, 8-oxo-2'-deoxynebularine, 8-oxo-2'-**deoxyinosine**, abasic sites, and a ring-opened adduct of C8-aminofluorene guanine. The C8 keto group of 8-oxodG:dC was present in the major groove and was correlated with tight binding (Kd = 8.9 nM). Binding was much weaker when the C8 keto functional group was in the minor groove, as in 8-oxodG:dA (Kd = 340 nM). The Km and Vmax values were detd. for the cleavage reaction. Specificity consts. (kcat/Km) were consistently higher for olidogeoxynucleotide duplexes contg. 8-oxopurines with C6 and C8 keto groups, as in 8-oxodG:dC and 8-oxodI:dC, where kcat/Km were 9.3 and 18 min-1 nM .times. 10-3, resp. 8-OxodN:dC lacked the C6 keto group; the specificity const. was 0.024 min-1 nM .times. 10-3. Taken together, the results suggested that the C8 keto group of 8-oxodeoxyguanine and the carbonyl moiety of formamidopyrimidine enable I to recognize and bind duplex DNA contg. these modified bases. An enzyme-catalyzed reaction involving the C6 keto group of the substrate led to removal of these lesions. A mechanism involving protonation at O6 of 8-oxoguanine was proposed to account for the N-glycosylase activity of I.

L12 ANSWER 51 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1994:185550 CAPLUS
DN 120:185550
TI Studies on the base pairing properties of **deoxyinosine** by solid phase hybridization to **oligonucleotides**
AU Case-Green, Stephen C.; Southern, Edwin M.
CS Dep. Biochem., Univ. Oxford, Oxford, OX1 3QU, UK
SO Nucleic Acids Res. (**1994**), 22(2), 131-6
CODEN: NARHAD; ISSN: 0305-1048
DT Journal
LA English
AB Extensive analyses of the base-pairing properties of **deoxyinosine** to A, C, G and T were carried out by measuring the hybridization of **oligonucleotides** with **deoxyinosine** in various positions to complementary sets of **oligonucleotides** made as an array on the surface of a glass microscope slide. With **deoxyinosine** in internal positions, results are consistent with previous studies, showing a preferential order for pairing of I-C > I-A > I-G .apprx. I-T. With 2 adjacent **deoxyinosines** in the center of the **oligonucleotide**, the order in duplex yield is CC > CA > AA > AC > GC > GA > CG > TA > TC > CT = AG > AT > GT > TT. With **deoxyinosine** at the ends of the **oligonucleotide**, at the 3' end there is the same order in duplex yield as for the **deoxyinosine** in internal positions, though with lower discrimination between the bases. When hybridization is carried out in TMACl there is little base pairing discrimination with **deoxyinosine**, or indeed any of the 4 natural bases at the 5' end. Changing the cation to Na+ increased discrimination slightly.

L12 ANSWER 52 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1994:99664 CAPLUS
DN 120:99664
TI Detailed study of sequence-specific DNA cleavage of triplex-forming

oligonucleotides linked to 1,10-phenanthroline
AU Shimizu, Miho; Inoue, Hideo; Ohtsuka, Eiko
CS Fac. Pharm. Sci., Hokkaido Univ., Sapporo, 060, Japan
SO Biochemistry (**1994**), 33(2), 606-13
CODEN: BICHAW; ISSN: 0006-2960
DT Journal
LA English
AB The authors introduced eight bases, including four base analogs, into 15-mer triplex-forming **oligonucleotides** (TFOs) [d-psTTTCTTTNTTTTCTT; ps = thiophosphate; N = A, G, C, T, 2'-**deoxyinosine** (I), 2'-deoxyxanthosine (X), 5-methyl-2'-**deoxycytidine** (m5C), or 5-bromo-2'-deoxyuridine (br5U)] to investigate the Hoogsteen-like hydrogen bonding to the base in the target 34-mer strand (d-TGAGTGAGTAAAGAAARAAAAGAATGAGTGCCAA.cntdot.d-TTGGCACTCATTCTTTTYTTTCTTTACTCACTCA; RY = AT, GC, TA, or CG). The authors examd. the thermal stability of 15-mer triplexes in buffer contg. 100 mM sodium acetate and 1 M NaCl at pH 5.0. The triplexes with typical triplets of T.cntdot.AT (51.3 .degree.C), br5U.cntdot.AT (52.4 .degree.C), C+.cntdot.GC (66.7 .degree.C), and m5C+.cntdot.GC (66.8 .degree.C) at the central position showed relatively higher Tm values, as expected. The relatively high stability of the X.cntdot.AT triplex (39.8 .degree.C) was obsd. Among the N.cntdot.TA triplets, G.cntdot.TA (44.8 .degree.C) was thermally the most stable, and moreover, the data showed that the N.cntdot.TA triplet was also stabilized by I in the N position (40.7 .degree.C). Furthermore, the TFOs were converted to DNA-cleaving mols. by introducing a newly synthesized 1,10-phenanthroline (OP) deriv. on the thiophosphate group at the 5' end. Cleavage reactions of the 32P-labeled DNA (34-mer) were carried out. The cleavage efficiencies were compared to the Tm values of triplexes with or without an OP deriv. Results showed that the increased cleavage yields reflect the higher thermal stability of the triplex formed in most cases, but a few exceptional cases existed. Esp., the G-contg. TFO did not show the above correlation between thermal stability and cleavage yield. The possibility of the binding of free Cu2+ ion to a G base or the formation of the 8-oxo-G base could explain the results. The influence of reducing agents on cleavage efficiency was also examd.

L12 ANSWER 53 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1994:99662 CAPLUS
DN 120:99662
TI Affinity crosslinking of duplex DNA by a pyrrole-**oligopeptide** conjugate
AU Sigurdsson, Snorri T.; Rink, Stacia M.; Hopkins, Paul B.
CS Dep. Chem., Univ. Washington, Seattle, WA, 98195, USA
SO J. Am. Chem. Soc. (**1993**), 115(26), 12633-4
CODEN: JACSAT; ISSN: 0002-7863
DT Journal
LA English
GI



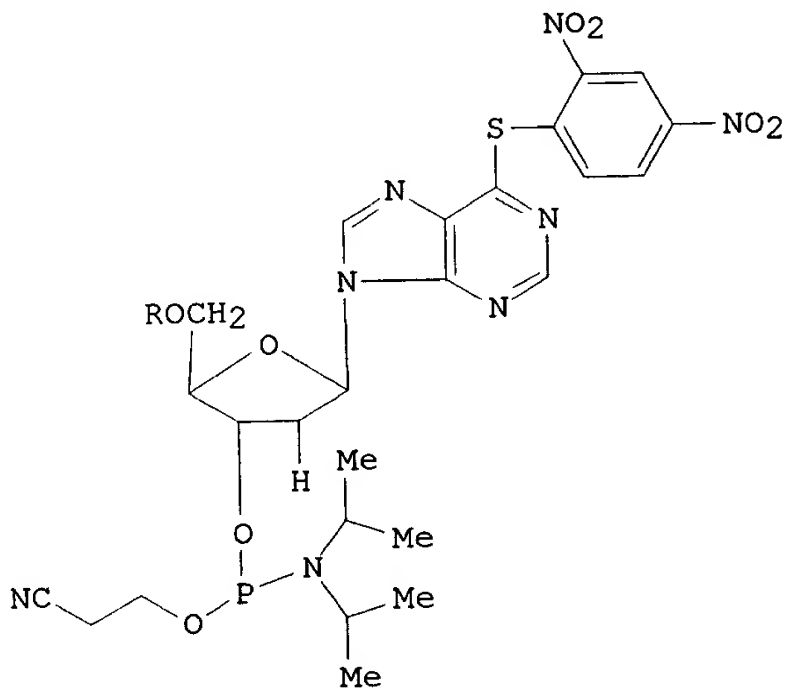
I

AB The short DNA sequences identified by clin. useful antitumor substances which act by [redacted]-DNA crosslinking are present [redacted] high frequency in genomes. The therapeutic strategy of targeting lower frequency sites requires the development of affinity crosslinking agents which select longer DNA sequences. The synthesis and in vitro reactions with duplex DNA of the DNA affinity interstrand and intrastrand crosslinking agent I are described. This substance is a conjugate of an **oligopeptide** which binds non-covalently and sequence specifically in the minor groove of DNA with a 2,3-bis(hydroxymethyl)pyrrole that cross-links duplex DNA by covalent reactions in the minor groove. At concns. as low as 10 nM, I was shown to efficiently interstrand cross-link a linearized plasmid. A comparable extent of reaction with an analog lacking the **oligopeptide** function (2,3-bis(hydroxymethyl)-1-methylpyrrole) was achieved only with a 1000-fold higher concn. Using a panel of self-complementary, synthetic DNA duplexes, it was shown that efficient crosslinking was achieved only when a sequence appropriate for non-covalent binding of the **oligopeptide** was adjacent to sites of covalent reaction for the pyrrole. Specifically, interstrand crosslinking was obsd. at the sequence 5'-d(CGAATT) and intrastrand crosslinking at the sequence 5'-d(GGAATT). Several lines of evidence suggest that these cross-links bridge the exocyclic amino groups of **deoxyguanosine** (dG) at 5'-d(CG) (interstrand) and 5'-d(GG) (intrastrand) sequences, including failure of **deoxyinosine** to substitute for dG in some reactions, depletion of dG in hydrolytic digests of inter- and intrastrand cross-linked samples, and direct observation in the hydrolyzates of a substance with MS properties expected for a conjugate of the crosslinking agent with two dG residues less two equiv. of water.

L12 ANSWER 54 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1993:642163 CAPLUS
DN 119:242163
TI The tetramethylammonium chloride method for screening of cDNA libraries using highly degenerate **oligonucleotides** obtained by backtranslation of amino-acid sequences
AU Honore, Bent; Madsen, Peder; Leffers, Henrik
CS Inst. Med. Biochem., Aarhus Univ., Aarhus, DK-8000, Den.
SO J. Biochem. Biophys. Methods (**1993**), 27(1), 39-48
CODEN: JBBMDG; ISSN: 0165-022X
DT Journal
LA English
AB The authors describe a method for screening of cDNA libraries with highly degenerate **oligonucleotides** using tetramethylammonium chloride (TMAC). This method is a convenient alternative to using probes generated by the polymerase chain reaction (PCR), esp. when these cannot easily be made. Nylon filters were prehybridized in buffered sodium chloride and hybridized with labeled **oligonucleotide** in buffer contg. 3M TMAC. In TMAC the melting temp. of the **oligonucleotide** is independent of the G + C content, thus only depending on the length. This was confirmed by the cloning of 13 specific cDNAs with G + C contents between 27 and 61% using 15-20-mer **oligonucleotides** with a degeneracy up to 512. The method was further improved for highly degenerate **oligonucleotides** by testing hybridization of four 18-mer **oligonucleotides**, each contg. one **deoxyinosine** (I) instead of A, G, C or T. **Oligonucleotides** contg. I pairing with A, G or T may have slightly lower melting temps. than those pairing with C. At practical circumstances all **oligonucleotides** hybridize about equally well at hybridization temps. 10.degree. below the irreversible melting temp. This was further confirmed by the cloning of four cDNAs with **oligonucleotides** contg. **deoxyinosines**

at 3 or 4 ambiguous positions.

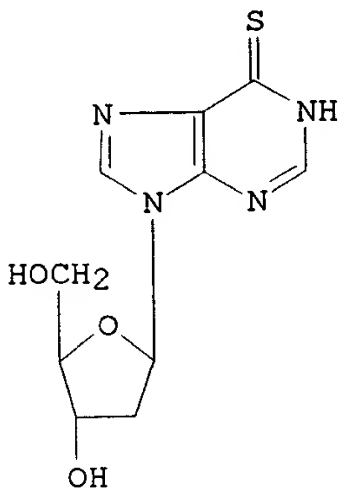
L12 ANSWER 55 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1993:581144 CAPLUS
DN 119:181144
TI Synthesis and duplex stability of **oligodeoxynucleotides** containing 6-mercaptopurine
AU Xu, Yao Zhong; Zheng, Qinguo; Swann, Peter F.
CS Dep. Biochem. Mol. Biol., Univ. Coll. London, London, WC1E 6BT, UK
SO Tetrahedron Lett. (**1992**), 33(39), 5837-40
CODEN: TELEAY; ISSN: 0040-4039
DT Journal
LA English
GI



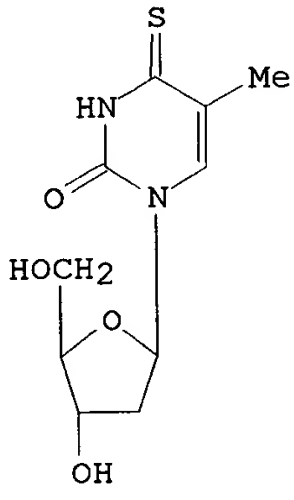
I

AB Simple procedures for conversion of 2'-**deoxyinosine** into 6-thio-2'-**deoxyinosine** and for prepn. of S-protected 6-mercaptopurine phosphoramidite I (R = 4,4'-dimethoxytrityl), are described. I was incorporated into DNA **oligomers** and converted into **oligomers** contg. 6-mercaptopurine and other purines modified at the 6-position. Measurements of the melting temp. of DNA duplexes contg. 6-merceptopurine or 6-thioguanine show that both preferentially pair with cytosine rather than with thymine, but that the presence of the S generally destabilizes the DNA duplex.

L12 ANSWER 56 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1993:581139 CAPLUS
DN 119:181139
TI Site-specific disulfide bridges in **oligodeoxyribonucleotide** duplexes containing 6-mercaptopurine and 4-thiothymine bases
AU Milton, John; Connolly, Bernard A.; Nikiforov, Theo T.; Cosstick, Richard
CS Dep. Chem., Robert Robinson Lab., Liverpool, UK
SO J. Chem. Soc., Chem. Commun. (**1993**), (9), 779-80
CODEN: JCCCAT; ISSN: 0022-4936
DT Journal
LA English
GI



I



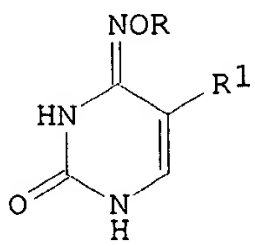
II

AB A self complementary **oligodeoxynucleotide** duplex contg. 6-thio-2'-**deoxyinosine** (I) and 4-thio-2'-**deoxythymidine** (II) undergoes crosslinking to form interstrand disulfide bridges under aerobic conditions. The reaction is reversed by dithiothreitol.

L12 ANSWER 57 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1993:575368 CAPLUS
DN 119:175368
TI PCR and hybridization with primers/probes containing purine analogs
IN Brown, Daniel McGillivray; Lin, Paul Yee Siew Kong Thoo
PA Medical Research Council, UK
SO PCT Int. Appl., 30 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9305175	A1	19930318	WO 1992-GB1661	19920911 <--
	W: AT, AU, BB, BG, BR, CA, CH, CS, DE, DK, ES, FI, GB, HU, JP, KP, KR, LK, LU, MG, MN, MW, NL, NO, PL, RO, RU, SD, SE, US				
	RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, SN, TD, TG				
	AU 9225442	A1	19930405	AU 1992-25442	19920911 <--
PRAI	GB 1991-19377		19910911		
	GB 1991-23187		19911101		
	WO 1992-GB1661		19920911		

OS MARPAT 119:175368
GI



I

AB **Oligonucleotides** contg. purine analogs I (R=H,Me; R'=H,CH2OH; R-R'=CH2CH2 forming a cyclic structure) can be used as primers for PCR and are more effective hybridization probes than conventional **oligonucleotide** mixts. Representative I are 3,4-dihydro-8H-pyrimido[4,5-C][1,2]oxazino-7-one (P), N6-methoxy-2,6-diaminopurine (K),

and **deoxyinosine** (I). Controlled-pore glass functionalized with 3'-O-succiny[redacted]'-DMT-P was prepd. and used in [redacted]epn. of I-contg. **oligonucleotides**. **Oligomers** with P at the 3' terminus were shown to function as primers in the PCR. **Oligomers** with several P, K, or P and K residues were also effective primers. Hybridization probes contg. P, P and K, or P and I were more effective than the corresponding **oligonucleotide** mixts.

L12 ANSWER 58 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1993:532916 CAPLUS
DN 119:132916
TI Use of predetermined nucleotides having altered base pairing characteristics in the amplification of nucleic acid molecules
IN Shuster, David M.; Rashtchian, Ayoub
PA Life Technologies, Inc., USA
SO PCT Int. Appl., 36 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9314217	A1	19930722	WO 1993-US109	19930108 <--
	W: CA, JP				
	RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
	US 5578467	A	19961126	US 1994-246921	19940520 <--
	US 5869251	A	19990209	US 1996-755736	19961125 <--
PRAI	US 1992-819132		19920110		
	US 1994-246921		19940520		

AB A method for improving nucleic acid amplification comprises equalizing the priming efficiency of the primers by incorporating .gtoreq.1 **deoxyinosine** residues into one or both primers.

L12 ANSWER 59 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1993:487447 CAPLUS
DN 119:87447
TI PCR with degenerate primers containing **deoxyinosine** fails with Pfu DNA polymerase
AU Knittel, Thomas; Picard, Didier
CS Dep. Biol. Cell., Univ. Geneve, Geneva, 1211, Switz.
SO PCR Methods Appl. (**1993**), 2(4), 346-7
CODEN: PMAPES; ISSN: 1054-9803
DT Journal
LA English
AB Pfu DNA polymerase use for amplifying a target sequence in PCR was studied. Degenerate sense and antisense **oligonucleotide** primers and **deoxyinosine**-contg. primers were tested. Pfu DNA polymerase cannot amplify a target sequence using **deoxyinosine**-contg. primers, however its lower error rate per nucleotide, compared with that of Taq DNA polymerase, makes it useful for PCR employing degenerate primers.

L12 ANSWER 60 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1993:449812 CAPLUS
DN 119:49812
TI Specific synthesis of adenosine(5')tetraphospho(5')nucleoside and adenosine(5')**oligophospho**(5')adenosine (n > 4) catalyzed by firefly luciferase
AU Ortiz, Begona; Sillero, Antonio; Gunther Sillero, Maria A.
CS Fac. Med., Univ. Auton. Madrid, Madrid, E-28029, Spain
SO Eur. J. Biochem. (**1993**), 212(1), 263-70
CODEN: EJBCAI; ISSN: 0014-2956
DT Journal
LA English

OS CASREACT 119:49812

AB Luciferase catalyzes the preferential synthesis of adenosine(5')tetraphospho(5')nucleoside (Ap4N) in the presence of luciferin (LH2), adenosine 5'-[.gamma.-thio]triphosphate (ATP[.gamma.S] and NTP (other than ATP), with very low, or undetectable synthesis of Ap4A or Np4N, because ATP[.gamma.S] is a good adenylyl donor for the formation of the E-LH2-AMP complex, but a poor adenylyl acceptor from the complex, and NTP, other than ATP, are bad nucleotidyl donors, but good acceptors of the AMP moiety of the E-LH2-AMP complex. Synthesis of the corresponding Ap4N (or Ap5G in the case of p4G were obtained in the presence of ATP[.gamma.S] and GTP, UTP, CTP, XTP, dTTP, ITP, dGTP, dCTP, dITP, .epsilon.ATP (.epsilon.A, N6-ethenoadenosine) or p4G. The yield of synthesis of AP4N was at least 50% of that theor. expected. The process can be easily scaled-up, which allows synthesis of at least 1-5 .mu.mol Ap4N. Further evidence for the synthesis of Ap4G from ATP[.gamma.S] and GTP was obtained by 1H-NMR and 31P-NMR spectroscopy. Synthesis of Ap4N, in yields lower than those above, can also be obtained in the presence of ADP and NTP; synthesis is due to the presence in com. luciferase of enzyme (adenylate kinase and NDP kinase) that catalyze the synthesis of ATP from ADP and NTP. In the presence of ATP and polyphosphate, luciferase catalyzes the synthesis of a variety of compds. of adenosine 5'-polyphosphates (pnA; n=3-20 and ApnA; n=4-16). In the presence of P3 of P4, preferential synthesis of p4A and Ap5A or p5A and Ap6A were obtained, resp., showing that both polyphosphates accept the adenylyl moiety of the E-LH2-AMP complex. Polyphosphates of chain length 5, 15 and 35 elicited the synthesis of a variety of PnA and ApnA. Ap4A is also split by luciferase in the presence of P3 or P4 (but not in the presence of P5) yielding preferential synthesis of p4A and Ap5A, or p5A and Ap6A, resp.

L12 ANSWER 61 OF 74 CAPLUS COPYRIGHT 2009 ACS

AN 1993:169517 CAPLUS

DN 118:169517

TI Aminolysis of 2'-**deoxyinosine** aryl ethers: nucleoside model studies for the synthesis of functionally tethered **oligonucleotides**

AU Ferentz, Ann E.; Verdine, Gregory L.

CS Dep. Chem., Harvard Univ., Cambridge, MA, 02143, USA

SO Nucleosides Nucleotides (**1992**), 11(10), 1749-63
CODEN: NUNUD5; ISSN: 0732-8311

DT Journal

LA English

AB Several O6-aryl-2'-**deoxyinosines** were synthesized and found to undergo conversion to N6-substituted-2'-deoxyaldenosines upon treatment with aq. amines. The kinetics for reaction of these nucleosides with various amines suggests that O6-phenyl- and O6-(p-nitrophenyl)-2'-**deoxyinosine** are suitable "convertible nucleoside" precursors for the site-specific introduction of functionally tethered 2'-**deoxyadenosines** into DNA.

L12 ANSWER 62 OF 74 CAPLUS COPYRIGHT 2009 ACS

AN 1992:571920 CAPLUS

DN 117:171920

TI Nucleosides and nucleotides 111. Thermal stability of **oligodeoxyribonucleotide** duplexes containing N6-hydroxyadenine in substitution for adenine

AU Nishio, Hisayoshi; Ono, Akira; Matsuda, Akira; Ueda, Tohru

CS Fac. Pharm. Sci., Hokkaido Univ., Sapporo, 060, Japan

SO Chem. Pharm. Bull. (**1992**), 40(5), 1355-9
CODEN: CPBTAL; ISSN: 0009-2363

DT Journal

LA English
AB An **oligodeox[redacted]bonucleotide** contg. N6-hydroxy[redacted]nine (H) has been synthesized. An order of melting temps. of duplexes consisting of 5'd(CCTGGTAHCAGGTCC)3':5d(GGACCTGNTACCAGG) (N = A, G, T, C) and H:T > H:G > H:A > H:C.

L12 ANSWER 63 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1992:442879 CAPLUS
DN 117:42879
TI Multinuclear nuclear magnetic resonance studies of sodium cation-stabilized complex formed by d(G-G-T-T-T-T-C-G-G) in solution. Implications for G-tetrad structures
AU Wang, Yong; De los Santos, Carlos; Gao, Xiaolian; Greene, Karen; Live, David; Patel, Dinshaw J.
CS Coll. Physicians Surg., Columbia Univ., New York, NY, 10032, USA
SO J. Mol. Biol. (**1991**), 222(3), 819-32
CODEN: JMOBAK; ISSN: 0022-2836
DT Journal
LA English
AB There has been much recent interest in the self-assocn. of short **deoxyguanosine**-rich motifs within single-stranded DNAs to generate monovalent cation modulated four-stranded helical segments called G-quadruplexes stabilized by hydrogen-bonded G-tetrad alignments. Here, structural aspects of this novel alignment are addressed and multinuclear 1H, 31P and 13C NMR studies reported on the d(G2T4CG2) deoxynonanucleotide with Na+ as counterion in aq. soln. at low temp. This sequence forms stable structures even through it cannot align by Watson-Crick hydrogen bond formation. The 4 narrow exchangeable protons detected between 11.5 and 12.0 parts ppm, which are common to the d(G2T4CG2) deoxynanucleotide and the d(G2TCG2) deoxyhexanucleotide sequences, are assigned to **deoxyguanosine** imino protons hydrogen-bonded to carbonyl acceptor groups. These narrow imino protons are not detected for d(IGN5IG) and d(I2N5G2), where two **deoxyguanosine** residues are replaced by two **deoxyinosine** residues in the deoxynonanucleotide sequences. This implies that the 2-amino protons of **deoxyguanosine** must also participate in hydrogen bond formation and stabilize the structured conformation of d(G2T4CG2) in Na cation-contg. soln. The base and sugar H1', H2',2'', H3', and H4' protons protons of the d(G2T4CG2) **oligomer** were completely assigned following anal. of two-dimensional nuclear Overhauser enhancement spectroscopy and two-dimensional correlated spectroscopy data sets in 0.1 M-NaCl, 10 mM sodium phosphate, 2H2O soln. at 0.degree.. The relative magnitude of the nuclear Overhauser enhancements (NOEs) between the base H8 and its own sugar H1' protons of individual **deoxyguanosine** residues establishes that G1 and G8 adopt syn orientations while G2 and G9 adopt anti orientations about the glycosidic bond in the d(G1-G2-T3-T5-T6-C7-G8-G9) sequence in both Na and K cation-contg. aq. soln. Consequently, any structure proposed for the tetramol. complex of d(G2T4CG2) must exhibit alternating G(syn) and G(anti) glycosidic torsion angles within each strand. The directionality and magnitude of the obsd. NOEs are consistent with the G(syn)-G(anti) steps adopting right-handed helical conformations in soln. Also, the H8 protons of G1 and G8 (7.35 to 7.45 p.p.m.) in a syn alignment are shifted significantly upfield from the H8 protons of G2 and G9 (8.0 to 8.3 p.p.m.) in an anti alignment. Two-dimensional proton-detected heteronuclear (1H-31P and 1H-13C) spectra have been recorded at natural abundance on the d(G2T4CG2) sequence in aq. soln. The phosphorus resonances are dispersed over 1.5 ppm with the G2-T3 and T6-C7 phosphates shifted to low field and the T4-T5 phosphate shifted to high field of the unperturbed spectral region. These results suggest that the pyrimidine-rich T4C segment in d(G2T4CG2) is involved either in hairpin

loop or in hairpin bulge formation. The base and sugar carbon resonances have been assigned and it is noted that the base, C1', C3' and C-4' carbons of G1 and G8 in a syn alignment resonate to low field of the corresponding carbon atoms of G2 and G9, which adopt an anti alignment. The NMR results are discussed in relation to proposed models for G-tetrad alignments of G-quadruplex structures.

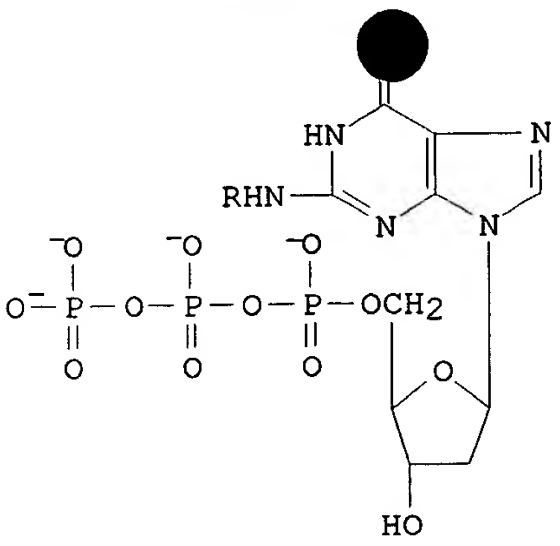
L12 ANSWER 64 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1992:402904 CAPLUS
DN 117:2904
TI Interstrand cross-linking of duplex DNA by nitrous acid: covalent structure of the dG-to-dG cross-link at the sequence 5'-CG
AU Kirchner, James J.; Sigurdsson, Snorri T.; Hopkins, Paul B.
CS Dep. Chem., Univ. Washington, Seattle, WA, 98195, USA
SO J. Am. Chem. Soc. (**1992**), 114(11), 4021-7
CODEN: JACSAT; ISSN: 0002-7863
DT Journal
LA English
AB It has previously been shown in synthetic **oligodeoxynucleotides** that the interstrand crosslinking reaction of nitrous acid with duplex DNA preferentially forms thermally and base-stable links between **deoxyguanosine** residues at the duplex sequence 5'-CG. The covalent nucleus of this linkage is shown herein to result from the presence of a residue in which the original deoxyguanosyl residues on opposite strands are crosslinked through a single N2 atom common to both [N2-(2-deoxyinosyl)**deoxyguanosine** residue]. Variation of nitrous acid concn., reaction time, and temp. established conditions under which up to a several percent yield of crosslinked **oligodeoxynucleotide** was obtained. Evidence for the covalent structure of the crosslink reported herein includes comparison of spectroscopic properties (mass spectrum, UV specta at 3 pH values, and 1H NMR spectrum) of N2-(2-deoxyinosyl)**deoxyguanosine** isolated by enzymic hydrolysis of crosslinked **oligodeoxynucleotides** to those of the same substance and its derivs. previously isolated from nitrous acid-treated calf thymus DNA. Further evidence in favor of crosslinking through N2 is reported: substitution of **deoxyinosine**, which lacks an N2 amino group, in place of **deoxyguanosine** at both sites in the duplex sequence 5'-CG abolishes dG-to-dG (dI-to-dI) crosslinking.

L12 ANSWER 65 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1992:129476 CAPLUS
DN 116:129476
TI Preparation of **oligonucleotides** containing dAICA using an unexpected side-reaction observed on a protected derivative of 2-aza-2'-**deoxyinosine**
AU Fernandez-Forner, Dolors; Eritja, Ramon; Bardella, Francesc; Ruiz-Perez, Catalina; Solans, Xavier; Giralt, Ernest; Pedroso, Enrique
CS Dep. Quim. Org., Univ. Barcelona, Barcelona, 08025, Spain
SO Tetrahedron (**1991**), 47(42), 8917-30
CODEN: TETRAB; ISSN: 0040-4020
DT Journal
LA English
AB Attempts of synthesis of **oligonucleotides** contg. 2-aza-1'-**deoxyinosine** protected with the N,N-diphenylcarbamoyl group are described. An unexpected behavior of the protected nucleoside can be used for the introduction of 5-amino-1-(.beta.-D-2'-deoxyribofuranosyl)imidazole-4-carboxamide (dAICA) in synthetic **oligonucleotides**.

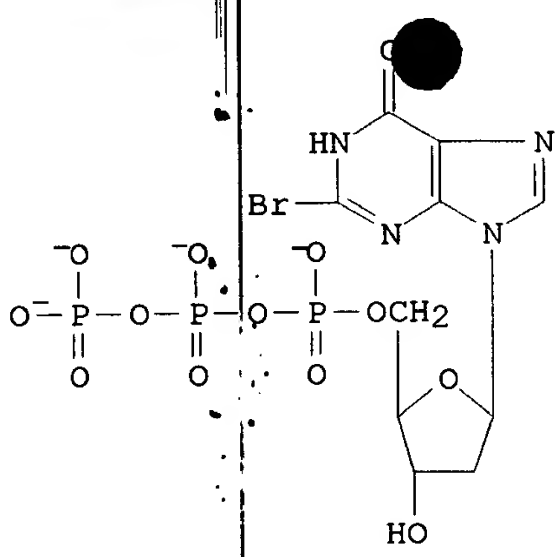
L12 ANSWER 66 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1992:120485 CAPLUS

DN 116:120485
TI Recognition [redacted]specific DNA sequences by mito[redacted]in C for alkylation
AU Kumar, Shiv; Lipman, Roselyn; Tomasz, Maria
CS Dep. Chem., City Univ. New York, New York, NY, 10021, USA
SO Biochemistry (**1992**), 31(5), 1399-407
CODEN: BICHAW; ISSN: 0006-2960
DT Journal
LA English
AB Synthetic **oligodeoxyribonucleotides** were reacted with mitomycin C (MC) under conditions which restricted MC to monofunctional alkylating activity. The yields of monofunctional alkylation of **oligonucleotides** with variable sequence were detd. by enzymic digestion of the reaction mixt. to unreacted nucleosides and the product of alkylation, a MC-**deoxyguanosine** adduct (I), followed by quant. anal. by HPLC. The relative yields of I reflected relative monoalkylation reactivities. They were compared in a series of **oligonucleotides** having the sequence 5'-NGN' in which the 5'-base was varied while the 3'-base was kept const. as T. Under Na2S2O4 activation conditions a striking enhancement of the yield was obsd. at the 5'-CG sequence: 36%, compared to 2% at 5'-AG and 4.1% at 5'-TG. The 5'-GG sequence also showed enhanced reactivity although to a lesser extent (14.7%). The enhancements were specific to the duplex state of the **oligonucleotides**. Using NADPH:cytochrome c reductase as the reducing agent gave similar results. MC activated by acidic pH also displayed 5'-CG alkylation specificity. 10-Decarbamoyl-MC activated by Na2S2O4 showed the same 5'-CG specificity as MC. Replacement of **deoxyguanosine** by **deoxyinosine** in the opposite strand at a 5'-CG site abolished the enhancement of alkylation. Such replacement at a 5'-GG site had a similar effect. The base 3' to the guanine had only a relatively modest modulating effect on the enhanced reactivity of the G at the 5'-CG sequence. This 3'-base effect appeared to be independent of the 5'-base of the 5'-NGN' triplet. The order of reactivity is 3'-(C > T > G > A). An explanation is proposed for the dominating 5'-CG (and, to a lesser extent, 5'-GG) specificity of the alkylation of DNA by MC, based primarily on the results of the inosine substitutions: At 5'-CG a H-bond is formed between the 2-amino group of guanine in the opposite strand and the 10-O atom of activated MC, facilitating alkylation at such sequence. An analogous mechanism applies at the 5'GG site. The 5'-CG and 5'-GG sites of DNA monoalkylation by MC coincide with the two crosslinkable sites (interstrand crosslink at CG.cntdot.CG and intrastrand crosslink at GC.cntdot.CC). The monoalkylation specificity may be a mol. evolutionary device to guide MC preferentially to guanines located in crosslinkable sequences of DNA.

L12 ANSWER 67 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1992:41953 CAPLUS
DN 116:41953
TI N2-Substituted-2'-**deoxyguanosine** 5'-triphosphates as substrates for E. coli DNA polymerase I
AU Freese, Stephen; Hoheisel, Jorg; Lehrach, Hans; Wright, George
CS Med. Sch., Univ. Massachusetts, Worcester, MA, 01655, USA
SO Nucleosides Nucleotides (**1991**), 10(7), 1507-24
CODEN: NUNUD5; ISSN: 0732-8311
DT Journal
LA English
GI



I



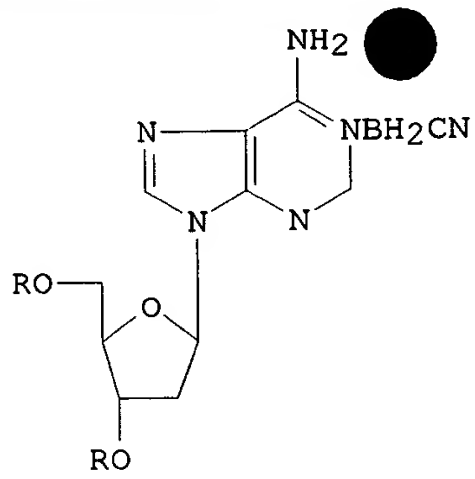
II

AB Several N2-alkyl I [R = Me, Et, CF3CH2), Me(CH2)5] and N2-Ph 2'-**deoxyguanosine** 5'-triphosphates I (R = Ph) and 2-bromo-2'-**deoxyinosine** 5'-triphosphate (II) were synthesized and tested as substrates for E. coli DNA polymerase I with a template:primer system requiring incorporation of 85 nucleotides. I (R = Me, Et) were found to be efficiently incorporated in place of dGTP to give full length product. I [R = (CH2)5Me] supported limited full length synthesis at high concn., but I (R = Ph) and I [R = C6H4(CH2)3Me-p] were poor substrates. II was a good substrate for polymerase I, and it was a replacement only for dGTP. Melting temps. of **oligodeoxyribonucleotides** contg. N2-alkyl-dG residues, annealed to complementary single stranded DNA, were lower than that of the normal **oligomer**.

L12 ANSWER 68 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1991:656567 CAPLUS
DN 115:256567
TI Preparation of boronated deoxynucleosides and **oligonucleotides** as drugs
IN Spielvogel, Bernard F.; Sood, Anup; Hall, Iris H.; Shaw, Barbara Ramsay
PA USA
SO PCT Int. Appl., 34 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 3

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9109048	A1	19910627	WO 1990-US7446	19901217 <--
	W: AU, CA, JP				
	RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LU, NL, SE				
	US 5130302	A	19920714	US 1989-453311	19891220 <--
	CA 2071936	AA	19910621	CA 1990-2071936	19901217 <--
	AU 9173448	A1	19910718	AU 1991-73448	19901217 <--
	AU 634450	B2	19930218		
	EP 506892	A1	19921007	EP 1991-905077	19901217 <--
	EP 506892	B1	19971008		
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE				
	JP 05507265	T2	19931021	JP 1991-505222	19901217 <--
	AT 159027	E	19971015	AT 1991-905077	19901217 <--
PRAI	US 1989-453311	19891220			
	WO 1990-US7446	19901217			

GI



I

AB Antitumor, antiinflammatory, and antilipemic cyanoborane adducts of 2'-deoxy nucleosides, e.g., I [R = H (II), protecting group] and **oligonucleotides** contg. at least one boronated nucleoside base were prepd. via O-protection of the 2'-deoxy nucleoside, reaction with LX (L = Lewis base; X = boron-contg. moiety), deprotection and optional phosphorylation and coupling with other nucleotides. 2'-**Deoxyadenosine** in DMF contg. imidazole was stirred 24 h at room temp. with ClSi(CHMe2)3 to give 3',5'-O-bis(triisopropylsilyl)-2'-**deoxyadenosine**, which was refluxed with Ph3PBH2CN for ca. 4 h to give 3',5'-O-bis(triisopropylsilyl)-2'-**deoxyadenosine** N7-cyanoborane [I; R = (CHMe2)3Si], which was stirred with Bu4NF in THF at room temp. to give II. II had an ED50 of 3.68 .mu.g/mL against L1210 lymphoid leukemia cells.

L12 ANSWER 69 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1991:601820 CAPLUS
DN 115:201820
TI Preferential recognition of I.cntdot.T base-pairs in the initiation of excision-repair by hypoxanthine-DNA glycosylase
AU Dianov, Grigory; Lindahl, Tomas
CS Imp. Cancer Res. Fund, Clare Hall Lab., South Mimms/Herts., EN6 3LD, UK
SO Nucleic Acids Res. (**1991**), 19(14), 3829-33
CODEN: NARHAD; ISSN: 0305-1048
DT Journal
LA English
AB Double-stranded synthetic **oligonucleotides** with a centrally located dIMP residue in a 5'-32P-labeled strand were employed as substrates for hypoxanthine-DNA glycosylase. The enzyme activity was monitored by the generation of a piperidine-sensitive site in the labeled **oligonucleotide**. The enzyme was purified approx. 5000-fold from calf thymus. The purified enzyme removed efficiently a hypoxanthine base residue from an I.cntdot.T base pair, but 15-20 times more slowly from an I.cntdot.C base pair. Similar results were obtained with **oligonucleotides** in which the **deoxyinosine** residue was placed in different surrounding nucleotide sequences. The enzyme had no detectable activity on mismatched G.cntdot.T, A.cntdot.G, or A.cntdot.C base pairs. The data indicate that hypoxanthine-DNA glycosylase participates in the repair of deaminated adenine residues in DNA.

L12 ANSWER 70 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1991:529735 CAPLUS
DN 115:129735
TI Quadruplex DNA formation in a region of the tRNA gene supF associated with hydrogen peroxide mediated mutations
AU Akman, Steven A.; Lingeman, Robert G.; Doroshow, James H.; Smith, Steven S.
CS City Hope Natl. Med. Cent., Duarte, CA, 91010, USA
SO Biochemistry (**1991**), 30(35), 8648-53

CODEN: BICHAW; ISSN: 0006-2960
DT Journal
LA English
AB A hot spot for H2O2/Fe-mediated mutation was obsd. between bases 154 and 170 of the supF gene in the mutation reporter plasmid pZ189 [Moraes et al. (1990), Akman et al. (1991)]. To further characterize this hot spot, the 33mer d(pAAAGTGATGGTGGTGGGGGAAGGATTCGAACCT) (pZ33), which is complementary to bases 159-191 of the supF gene, was synthesized. PZ33 annealed spontaneously in 10 mM Tris-HCl (pH 8.0)-1 mM EDTA-100 mM NaCl at 50.degree. into two major forms, one of which migrates more slowly than does d(pT)33 on nondenaturing 12% polacrylamide gels. Apparently, this form is a four-stranded structure stabilized by Hoogsteen-type **deoxyguanosine** quartets involving all **deoxyguanosines** of the sequence d(pGGTGGTGGGGG). PZ33 migrates as a single form that comigrates with d(pT)33 on denaturing 20% acrylamide-8M urea gels. Annealing an equimolar mixt. of 5'-32P-labeled pZ33 and the **oligodeoxynucleotide** d(pTTTTTTTTpZ33TTTTTTTT) (pZ49), as well as 5'-32P-labeled pZ49 and pZ33, caused the formation of four, discreet slowly migrating bands on nondenaturing 12% polyacrylamide gels. Mixing 5'-32P-labeled pZ33 with 5'-32P-labeled pZ49 resulted in five slowly migrating bands. An **oligodeoxynucleotide** identical with pZ33 except that every **deoxyguanosine** has been replaced with **deoxyinosine** did not anneal into a slowly migrating form. Di-Me sulfate protection studies demonstrated that all **deoxyguanosines** of the sequence d(pGGTGGTGGGGG) were protected at N-7 in the slowly migrating form but not in single-stranded pZ33. These data suggest that a hot spot for H2O2/Fe-mediated base substitutions is located adjacent to a sequence that can spontaneously adopt a quadruplex structure in which **deoxyguanosine** quartets are Hoogsteen bonded.

L12 ANSWER 71 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1991:423592 CAPLUS
DN 115:23592
TI Acid phosphatase-11, a tightly linked molecular marker for root-knot nematode resistance in tomato: from protein to gene, using PCR and degenerate primers containing **deoxyinosine**
AU Aarts, Jac M. M. J. G.; Hontelez, Jan G. J.; Fischer, Peter; Verkerk, Ruud; Van Kammen, Albert; Zabel, Pim
CS Dep. Mol. Biol., Agric. Univ., Wageningen, NL-6703 HA, Neth.
SO Plant Mol. Biol. (**1991**), 16(4), 647-61
CODEN: PMBIDB; ISSN: 0167-4412
DT Journal
LA English
AB To cloning the root-knot nematode resistance gene Mi in tomato by chromosome walking, a mol. probe was developed for the tightly linked acid phosphatase-1 (Aps-1) locus. The acid phosphatase-1 allozyme (APS-11), encoded by the Aps-11 allele originating from Lycopersicon peruvianum, was purified to apparent homogeneity from tomato roots and suspension cells. Microsequencing of CNBr and tryptic peptides generated from APS-11 provided a partial amino acid sequence, which accounted for approx. 23% of the protein and revealed 2 stretches of homol. with soybean proteins KSH3 and VSP27, comprising 22 matches within 26 amino acid residues. The partial amino acid sequence information enabled us to isolate a 2.4 kb genomic Aps-11 sequence by means of the polymerase chain reaction (PCR), primed by degenerate pools of **oligodeoxyribonucleotides**, synthesized on the basis of the amino acid sequences. Synthesis of the 2.4 kb PCR product was specific for genomic templates carrying the L. peruvianum Aps-11 allele. Crucial to the priming specificity and the synthesis of the 2.4 kb genomic sequence was the use of degenerate primer

pools in which the no. of different primer species was limited by incorporating **deoxyinosine** phosphate residues at 3 and 4 base ambiguities. In using cDNA as a template, a 490 bp sequence was obtained, indicating a high proportion of intron sequences in the 2.4 kb genomic Aps-11 sequence. The Aps-11 origin of the PCR product was confirmed by RFLP (restriction fragment length polymorphism) anal., using both a chromosome 6 substitution line and a pair of nearly isogenic lines, differing for a small chromosomal region around the Aps-1/Mi loci.

L12 ANSWER 72 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1991:56965 CAPLUS
DN 114:56965
TI DNA sequencing by multiple mixed **oligonucleotide** probes
IN Macevicz, Stephen C.
PA DNAX Research Institute of Molecular and Cellular Biology, Inc., USA
SO PCT Int. Appl., 39 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9004652	A1	19900503	WO 1989-US4741	19891023 <--
	W: JP				
	RW: AT, BE, CH, DE, FR, GB, IT, LU, NL, SE				
	US 5002867	A	19910326	US 1988-261702	19881024 <--
	EP 439550	A1	19910807	EP 1989-912884	19891023 <--
	R: AT, BE, CH, DE, FR, GB, IT, LI, LU, NL, SE				
	JP 04501362	T2	19920312	JP 1990-500627	19891023 <--
PRAI	US 1988-261702	19881024			
	US 1988-186053	19880425			
	WO 1989-US4741	19891023			

AB The procedure was applied to the sequence detn. of the 119 bp Sca-Xmn fragment of pUC19 using B-mer probes as well as the 323 bp PvuII fragment of pUC19 using 9-mer probes.

L12 ANSWER 73 OF 74 MEDLINE
AN 1998290311 MEDLINE
DN 98290311
TI Studies on the synthesis of **oligonucleotides** containing photoreactive nucleosides: 2-azido-2'-**deoxyinosine** and 8-azido-2'-**deoxyadenosine**.
AU F`abrega C; Guimil Garcia R; Diaz A R; Eritja R
CS European Molecular Biology Laboratory, Heidelberg, Germany.
SO BIOLOGICAL CHEMISTRY, **(1998 Apr-May)** 379 (4-5) 527-33.
Journal code: CK4. ISSN: 1431-6730.
CY GERMANY: Germany, Federal Republic of
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199810
EW 19981003
AB **Oligonucleotides** containing the photoreactive nucleosides 2-azido-2'-**deoxyinosine** and 8-azido-2'-**deoxyadenosine** have been prepared using protected 2-fluoro-2'-**deoxyinosine** and 8-bromo-2'-**deoxyadenosine** phosphoramidites. After the assembly of the **oligonucleotides**, the nucleoside derivatives are converted to the corresponding azido derivatives by treatment with lithium azide in dry DMF. Deprotection of **oligonucleotides** carrying these azidonucleosides is performed with concentrated ammonia at room temperature.

L12 ANSWER 74 OF 74 MEDLINE

AN 97169228 MEDLINE
DN 97169228
TI Selective amplification of RNA utilizing the nucleotide analog dITP and Thermus thermophilus DNA polymerase.
AU Auer T; Sninsky J J; Gelfand D H; Myers T W
CS Program in Core Research, Roche Molecular Systems, Alameda, CA 94501, USA.
SO NUCLEIC ACIDS RESEARCH, **(1996 Dec 15)** 24 (24) 5021-5.
Journal code: O8L. ISSN: 0305-1048.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 199705
AB The ability to selectively amplify RNA in the presence of genomic DNA of analogous sequence is cumbersome and requires implementation of critical controls for genes lacking introns. The convenient approaches of either designing **oligonucleotide** primers at the splice junction or differentiating the target sequence based on the size difference obtained by the presence of the intron are not possible. Our strategy for the selective amplification of RNA targets is based on the enzymology of a single thermostable DNA polymerase and the ability to modulate the strand separation temperature requirements for PCR amplification. Following reverse transcription of the RNA by recombinant Thermus thermophilus DNA polymerase (rTth pol), the resulting RNAxDNA hybrid is digested by the RNase H activity of rTth pol, allowing the PCR primer to hybridize and initiate second-strand cDNA synthesis. Substitution of one or more conventional nucleotides with nucleotide analogs that decrease base stacking interactions and/or hydrogen bonding (e.g. hydroxymethyldUTP or dITP) during the first- and second-strand cDNA synthesis step reduces the strand separation temperature of the resultant DNAxDNA duplex. Alteration of the thermal cycling parameters of the subsequent PCR amplification, such that the strand separation temperature is below that required for denaturation of genomic duplex DNA composed of standard nucleotides, prevents the genomic DNA from being denatured and therefore amplified.

L15 ANSWER 1 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 2000:201085 CAPLUS
DN 132:247112
TI Detection of genes and alleles associated with disease by mass spectrometric detection of nucleic acid hybridization
IN Koster, Hubert; Higgens, G. Scott; Little, Daniel P.
PA Sequenom, Inc., USA
SO U.S., 95 pp., Cont.-in-part of Ser. No. US 1995-406199, filed on 17 Mar 1995, now
CODEN: USXXAM
DT Patent
LA English
FAN.CNT 5

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 6043031	A	20000328	US 1996-617256	19960318 <--
	US 5605798	A	19970225	US 1995-406199	19950317 <--
PRAI	US 1995-406199	19950317			
	US 1993-1323	19930107			
	US 1994-178216	19940106			

AB The invention provides fast and highly accurate mass spectrometer based processes for detecting a particular nucleic acid sequence in a biol. sample. Depending on the sequence to be detected, the processes can be used, for example, to diagnose a genetic disease or chromosomal abnormality; a predisposition to a disease or condition, infection by a pathogenic organism, or for detg. identity or heredity. The method uses mass spectrometry to detect the formation of hybrids. The target sequence is first captured using an immobilized capture probe and the captured sequences are then interrogated with a set of probes, e.g. allele-specific probes that are differentially labeled, and the probes that are captured are characterized. Samples are then conditioned to minimize the charge on the nucleic acids and then analyzed by mass spectrometry. Further, 7-deazapurines may be used in prepn. of amplification products to lower the risk of depurination. Use of the method to identify mutant alleles of a no. of human genes and to detect pathogens is demonstrated.

RE.CNT 29
RE
(2) Anon; WO 8909282 1989 CAPLUS
(3) Anon; WO 8909282 1989 CAPLUS
(4) Anon; WO 8912694 1989 CAPLUS
(5) Anon; WO 8912694 1989 CAPLUS
(6) Anon; EP 0360677 A1 1990 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L15 ANSWER 2 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1998:696939 CAPLUS
DN 129:299898
TI A trans-platinum based compound, a diagnostic kit comprising said compound and a method for labeling a bio-organic molecule wherein use is made of said compound
IN Houthoff, Hendrik Jan; Reedijk, Jan; Jelsma, Tinka; Heetebrij, Rob J.; Volkers, Herman H.
PA Kreatech Biotechnology B.V., Neth.

SO Eur. Pat. Appl., 11 pp.
CODEN: EPXXD
DT Patent
LA English
FAN.CNT 2

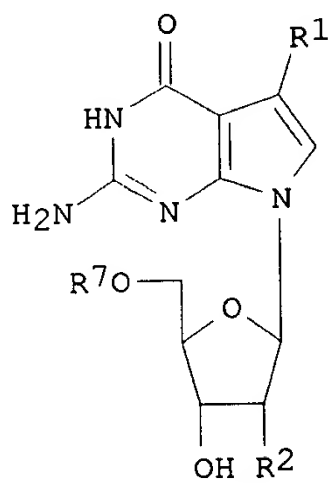
	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	EP 870770	A1	19981014	EP 1997-201066	19970410 <--
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
	EP 973785	A1	20000126	EP 1998-912826	19980409 <--
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, NL, SE, PT, IE, FI				

PRAI EP 1997-201066 19970410
WO 1998-N
L206 19980409
OS MARPAT 129:299898
AB The present invention is concerned with a trans-platinum based compd. for use in a method for labeling a bio-org. mol. The syntheses and applications of several platinum based compds. are presented. The incorporation of representative compds. into DNA is illustrated.

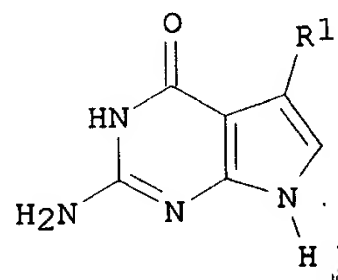
L15 ANSWER 3 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1998:629981 CAPLUS
DN 129:260742
TI Preparation of 7-deaza-2'-**deoxyguanosine-5'-triphosphate** derivatives and their use in DNA sequencing
IN Fuller, Carl; McDougall, Mark; Kumar, Shiv
PA Amersham Pharmacia Biotech Inc, USA
SO Eur. Pat. Appl., 20 pp.
CODEN: EPXXDW
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	EP 866070	A1	19980923	EP 1998-301727	19980309 <--
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
	GB 2323357	A1	19980923	GB 1998-5000	19980309 <--
	GB 2323357	B2	19990929		
	JP 2000119296	A2	20000425	JP 1998-72317	19980320 <--

PRAI US 1997-41320 19970320
OS MARPAT 129:260742
GI



I



II

AB The title compds. (I; R1 = C1-10 alkyl optionally substituted with OH,

amino, C1-4 alkoxy or halo; R2 = H, OH; R7 = H, mono-, di-, triphosphate or thiophosphate group; when R1 = Me then R7 = (deoxy)teq. H), useful, e.g., in resoln. of compression artifacts in DNA sequencing, were prepd. A **nucleotide** sequence contg. I, a DNA acid sequence contg. a base II (R1 = C1-10 alkyl, optionally substituted by OH, amino, C1-4 alkoxy or halo), a method for detg. the nucleoside base sequence of a DNA mol., a method of elongation of an **oligonucleotide** sequence, and 7-alkynyl analogs of I are also claimed. For example, esterification of 7-(prop-1-ynyl)-7-deaza-2'-**deoxyguanosine** and hydrogenation of the resulting **5'-triphosphate** ester Et3N-salt with H in the presence of Pd/C gave I (R1 = Pr, R2 = H, R7 = triphosphate group), useful for the title purpose.

L15 ANSWER 4 OF 74 CAPLUS COPYRIGHT 2000 ACS DUPLICATE 1
AN 1998:485882 CAPLUS
DN 129:227375
TI Misincorporation of 2'-Deoxyoxanosine **5'-Triphosphate** by DNA Polymerases and Its Implication for Mutagenesis
AU Suzuki, Toshinori; Yoshida, Mitsuo; Yamada, Masaki; Ide, Hiroshi; Kobayashi, Mutsumi; Kanaori, Kenji; Tajima, Kunihiko; Makino, Keisuke
CS Institute of Advanced Energy, Kyoto University, Gokasho, Uji, 611-0011, Japan
SO Biochemistry (**1998**), 37(33), 11592-11598
CODEN: BICHAW; ISSN: 0006-2960
PB American Chemical Society
DT Journal
LA English
AB 2'-Deoxyoxanosine (dOxo) is a novel DNA lesion produced by the reaction of 2'-**deoxyguanosine** (dGuo) with nitrous acid and nitric oxide [Suzuki, T., Yamaoka, R., Nishi, M., Ide, H., and Makino, K. (1996) J. Am. Chem. Soc. 118, 2515-2516]. In this work, 2'-deoxyoxanosine **5'-triphosphate** (dOTP) was prepd. by nitrous acid treatment of 2'-**deoxyguanosine 5'-triphosphate** (dGTP), and its incorporation into DNA by DNA polymerases was investigated to elucidate the substrate and mutagenic properties of dOTP. Primed M13mp18 DNA was replicated by Escherichia coli DNA polymerase I Klenow fragment (Pol I Kf) in the presence of three normal dNTPs and dOTP or 2'-deoxyxanthosine **5'-triphosphate** (dXTP), another major product of reaction of dGTP with nitrous acid and nitric oxide. DOTP substituted for dGTP and to a lesser extent for dATP, while dXTP substituted slightly for dGTP but not for dATP. Neither dOTP nor dXTP substituted for dCTP and dTTP. The similar results were obtained for the incorporation by T7 DNA polymerase deficient in 3'-5' exonuclease [T7(exo-)]. To quantify the substitution efficiency, kinetic parameters for incorporation of dOTP and dXTP opposite template C or T by Pol I Kf (exo-) were detd. and compared with those for dGTP using **oligodeoxynucleotide** templates. Incorporation efficiencies (f = Vmax/Km) of dOTP (f = 0.28% min-1 .mu.M-1) and dXTP (f = 0.10% min-1 .mu.M-1) opposite template C were much lower than that of dGTP (f = 1506% min-1 .mu.M-1). Frequencies of mutagenic incorporation of dOTP opposite template T were dependent on the nearest neighbor base pairs, and 1.6-3.9-fold higher than those for dGTP with the nearest neighbors contg. G.cntdot.C pairs. DXTP was not incorporated opposite template T with all four nearest neighbors. These data suggest that formation of dOTP, but not dXTP, from dGTP with nitrous acid or nitric oxide in the intracellular **nucleotide** pool would result in the elevation of the mutation frequency.

L15 ANSWER 5 OF 74 MEDLINE
AN 1998313272 MEDLINE

DN 98313272
TI Chromium(III) decreases the fidelity of human DNA polymerase beta.
AU Singh J; Snow E T
CS Nelson Institute of Environmental Medicine, New York University Medical Center, Tuxedo 10987, USA.
NC ES00260 (NIEHS)
CA13343 (NCI)
ES06498 (NIEHS)
SO BIOCHEMISTRY, **(1998 Jun 30)** 37 (26) 9371-8.
Journal code: A0G. ISSN: 0006-2960.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199809
EW 19980904
AB Certain particulate compounds of hexavalent chromium are well-known occupational and environmental human carcinogens. Hexavalent chromium primarily enters the cells and undergoes metabolic reduction; however, the ultimate trivalent oxidation state of chromium, Cr(III), predominates within the cell. DNA-bound Cr(III) has been previously shown to decrease the fidelity of replication in the M13 phage mutation assay. This study was done to understand how Cr(III), in the presence of physiological concentrations of magnesium, affects the kinetic parameters of steady-state DNA synthesis in vitro across site-specific O6-methylguanine (m6dG) residues by DNA polymerase beta (pol beta). Cr(III) binds to the short **oligomer** templates in a dose-dependent manner and stimulates the activity of pol beta. Cr(III) stimulates the mutagenic incorporation of dTTP opposite m6dG more than the nonmutagenic incorporation of dCTP, and thereby Cr(III) further decreases the fidelity of DNA synthesis across m6dG by pol beta. In contrast, Cr(III) does not affect the fidelity of DNA synthesis across the normal template base, dG. Both the enhanced activity and the mutagenic lesion bypass in the presence of Cr(III) may be associated with Cr(III)-dependent stimulation of pol beta binding to DNA as reported here. This study shows some of the mechanisms by which mutagenic chromium affects DNA synthesis.

L15 ANSWER 6 OF 74 MEDLINE
AN 1998139101 MEDLINE
DN 98139101
TI Efficient gap repair catalyzed in vitro by an intrinsic DNA polymerase activity of human immunodeficiency virus type 1 integrase.
AU Acel A; Udashkin B E; Wainberg M A; Faust E A
CS Lady Davis Institute for Medical Research, Sir Mortimer B. Davis-Jewish General Hospital and McGill AIDS Center, McGill University, Montreal, Quebec, Canada.
SO JOURNAL OF VIROLOGY, **(1998 Mar)** 72 (3) 2062-71.
Journal code: KCV. ISSN: 0022-538X.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 199805
EW 19980502
AB Cleavage and DNA joining reactions, carried out by human immunodeficiency virus type 1 (HIV-1) integrase, are necessary to effect the covalent insertion of HIV-1 DNA into the host genome. For the integration of HIV-1 DNA into the cellular genome to be completed, short gaps flanking the integrated proviral DNA must be repaired. It has been widely assumed that host cell DNA repair enzymes are involved. Here we report that HIV-1 integrase multimers possess an intrinsic DNA-dependent DNA polymerase activity. The activity was characterized by its dependence on Mg2+, resistance to N-ethylmaleimide, and inhibition by 3'-azido-2',3'-

dideoxythymidine-**5'-triphosphate**, coumermycin A1, and pyridoxal 5'-phosphate. The enzyme efficiently utilized poly(dA)-**oligo**(dT) or self-annealing **oligonucleotides** as a template primer but displayed relatively low activity with gapped calf thymus DNA and no activity with poly(dA) or poly(rA)-**oligo**(dT). A monoclonal antibody binding specifically to an epitope comprised of amino acids 264 to 273 near the C terminus of HIV-1 integrase severely inhibited the DNA polymerase activity. A deletion of 50 amino acids at the C terminus of integrase drastically altered the gel filtration properties of the DNA polymerase, although the level of activity was unaffected by this mutation. The DNA polymerase efficiently extended a hairpin DNA primer up to 19 **nucleotides** on a T20 DNA template, although addition of the last **nucleotide** occurred infrequently or not at all. The ability of integrase to repair gaps in DNA was also investigated.

We designed a series of gapped molecules containing a single-stranded region flanked by a duplex U5 viral arm on one side and by a duplex nonviral arm on the other side. Molecules varied structurally depending on the size of the gap (one, two, five, or seven **nucleotides**), their content of T's or C's in the single-stranded region, whether the CA dinucleotide in the viral arm had been replaced with a nonviral sequence, or whether they contained 5' AC dinucleotides as unpaired tails. The results indicated that the integrase DNA polymerase is specifically designed to repair gaps efficiently and completely, regardless of gap size, base composition, or structural features such as the internal CA dinucleotide or unpaired 5'-terminal AC dinucleotides. When the U5 arm of the gapped DNA substrate was removed, leaving a nongapped DNA template-primer, the integrase DNA polymerase failed to repair the last **nucleotide** in the DNA template effectively. A post-gap repair reaction did depend on the CA dinucleotide. This secondary reaction was highly regulated. Only two **nucleotides** beyond the gap were synthesized, and these were complementary to and dependent for their synthesis on the CA dinucleotide. We were also able to identify a specific requirement for the C terminus of integrase in the post-gap repair reaction. The results are consistent with a direct role for a heretofore unsuspected DNA polymerase function of HIV-1 integrase in the repair of short gaps flanking proviral DNA integration intermediates that arise during virus infection.

L15 ANSWER 7 OF 74 MEDLINE
AN 1998373657 MEDLINE
DN 98373657
TI Use of 5-nitroindole-2'-deoxyribose-**5'-triphosphate** for labelling and detection of **oligonucleotides**.
AU Smith C L; Simmonds A C; Hamilton A L; Martin D L; Lashford A G; Loakes D; Hill F; Brown D M
CS Amersham International plc, Amersham Laboratories, Buckinghamshire, UK.
SO NUCLEOSIDES AND NUCLEOTIDES, **(1998 Jan-Mar)** 17 (1-3) 555-64. Journal code: C5G. ISSN: 0732-8311.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199811
EW 19981103
AB The **5'-triphosphate** of 5-nitroindole-2'-deoxyriboside has been shown to be a good substrate for terminal deoxynucleotidyl transferase (TdT). An antibody has been prepared for the detection of 5-nitroindole and has been used for the detection of 5-nitroindole tailed DNA both in single-stranded form and after hybridisation to a template. This is therefore a new method for the detection of nucleic acid probes.

L15 ANSWER 8 OF [redacted] MEDLINE
AN 1998002694 MEDLINE
DN 98002694
TI Synergistic inhibition of HIV-1 reverse transcriptase by combinations of chain-terminating **nucleotides**.
AU Villahermosa M L; Martinez-Irujo J J; Cabodevilla F; Santiago E
CS Department of Biochemistry and Molecular Biology, University of Navarra, 31080 Pamplona, Spain.
SO BIOCHEMISTRY, **(1997 Oct 28)** 36 (43) 13223-31.
Journal code: A0G. ISSN: 0006-2960.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199801
EW 19980104
AB Synergistic inhibition of HIV replication in cell culture has been reported for many combinations of reverse transcriptase inhibitors. However, the biochemical basis underlying this interaction is in most cases unknown. It has been previously shown that combinations of L-697,661 or U-90152s with AZT or ddC synergistically inhibit HIV-1 replication in cell culture. The combination of AZT with ddC is also favorable with respect to the inhibition of viral replication. However, the corresponding combinations showed no synergy in inhibiting enzyme activity when tested on conventional polymerase assays using homo- or heteropolymeric RNA and DNA as template. Data obtained suggest that amplification of the effect of chain terminators, a consequence of the high potential number of termination sites present on the template, override the synergistic effect expected for the combination of two independent **nucleotide** analogs. When a saturating amount of enzyme over template:primer was used, and a single site on the template was available for each chain terminator, the combination of AZTTP and ddCTP synergistically inhibited enzyme activity, whereas, as expected, the combination of AZTTP and ddTTP behaved as merely additive. Under similar conditions the combination of U-90152s and AZTTP was also synergistic. These results suggest that synergy found in antiviral assays with combinations having nucleosidic inhibitors is not related to the synergistic inhibition of reverse transcriptase and might be due to the presence in the viral population of virus strains with different sensitivity to the inhibitors.

L15 ANSWER 9 OF 74 MEDLINE
AN 97238901 MEDLINE
DN 97238901
TI Stereoisomers of deoxynucleoside **5'-triphosphates** as substrates for template-dependent and -independent DNA polymerases.
AU Semizarov D G; Arzumanov A A; Dyatkina N B; Meyer A; Vichier-Guerre S; Gosselin G; Rayner B; Imbach J L; Krayevsky A A
CS Engelhardt Institute of Molecular Biology, Russian Academy of Sciences, 32 Vavilov Street, Moscow, 117984 Russia.
SO JOURNAL OF BIOLOGICAL CHEMISTRY, **(1997 Apr 4)** 272 (14) 9556-60.
Journal code: HIV. ISSN: 0021-9258.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals

EM 199707
AB All four pos[redacted]le stereoisomers of dNTP with [redacted]ard to deoxyribofuranose C-1' and C-4' carbon atoms were studied as substrates for several template-dependent DNA polymerases and template-independent terminal deoxynucleotidyl transferase. It was shown that DNA polymerases alpha, beta, and epsilon from human placenta and reverse transcriptases of human immunodeficiency virus and avian myeloblastosis virus incorporate into the DNA chain only natural beta-D-dNTPs, whereas calf thymus terminal deoxynucleotidyl transferase incorporates two **nucleotide** residues of alpha-D-dNTP and extends the resulting **oligonucleotide** in the presence of beta-D-dNTPs. The latter enzyme also extended alpha-anomeric D-**oligodeoxynucleotide** primers in the presence of beta-D-dNTPs. None of the studied enzymes utilized L-dNTPs. These data indicate that template-dependent DNA polymerases are highly stereospecific with regard to dNTPs, whereas template-independent terminal deoxynucleotidyl transferase shows less stereodifferentiation. It is likely that the active center of the latter enzyme forms no specific contacts with the nucleic bases of both **nucleotide** substrate and **oligonucleotide** primer.

L15 ANSWER 10 OF 74 MEDLINE
AN 97225986 MEDLINE
DN 97225986
TI Point mutations at the purine nucleoside phosphorylase locus impair thymocyte differentiation in the mouse.
AU Snyder F F; Jenuth J P; Mably E R; Mangat R K
CS Department of Medical Genetics, Faculty of Medicine, University of Calgary, AB Canada.
SO PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, **(1997 Mar 18)** 94 (6) 2522-7.
Journal code: PV3. ISSN: 0027-8424.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
OS GENBANK-L11290; GENBANK-U35374
EM 199706
EW 19970604
AB Three point mutations on the Np(b) allele of the purine nucleoside phosphorylase locus in the mouse have been recovered by male germ cell mutagenesis. The mutants were backcrossed, 12-14 generations, and are designated in increasing order of severity of enzyme deficiency and phenotype: B6-NPE, Met-87 --> Lys; B6-NPF, Ala-228 --> Thr; and B6-NPG, Trp-16 --> Arg. A marked decline in total cell numbers per thymus occurs between 2 and 3 months for the more severe B6-NPF and B6-NPG mutants (35% and 52%, respectively) and by 8 months for the less severe B6-NPE mutation. The thymocyte population is thereafter characterized by a 3- or 8-fold expanded precursor, CD4-CD8- double-negative population and 15% or 55% reduced CD4+CD8+ double-positive cells for the B6-NPF and B6-NPG strains, respectively. Spleen lymphocyte Thy-1+ cells are reduced by 50% and spleen lymphocyte response to T cell mitogen and interleukin 2 is reduced by 80%. Increases of thymocyte dGTP pools of 5- and 2.5-fold for B6-NPF and B6-NPG mutants, respectively, are observed. The purine nucleoside phosphorylase-deficient mouse exhibits age-dependent progressive perturbations in thymocyte differentiation, reduced numbers of thymocytes, and reduced splenic T cell numbers and response. The progressive T cell deficit is similar to the human disorder.

L15 ANSWER 11 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1998:138049 CAPLUS
DN 128:144887
TI Partial characterization of the dissolved organic phosphorus pool in the

oligotrophic North Pacific Ocean
AU Karl, David [redacted] Yanagi, Katsumi
CS Department of Oceanography, School of Ocean and Earth Science and Technology, University of Hawaii, Honolulu, HI, 96822, USA
SO Limnol. Oceanogr. (**1997**), 42(6), 1398-1405
CODEN: LIOCAH; ISSN: 0024-3590
PB American Society of Limnology and Oceanography
DT Journal
LA English
AB The application of 2 independent methods to det. P in seawater, continuous-flow UV photodecompn. and Mg-induced copptn., provided a partial characterization of the dissolved P pools at Station ALOHA (22.degree.45'N, 158.degree.W) in the **oligotrophic** subtropical North Pacific Ocean. Comprehensive lab. analyses of the UV light-induced photodecompn. of a variety of specific org. P compds. dissolved in seawater confirmed that sub-micro-molar concns. of monophosphate compds. could be anal. sepd. from **nucleotide** di- and triphosphates, based on a previously described temp.-controlled low-pressure, Hg vapor UV irradn. treatment. When combined with a recently described high-precision P-detection system, seawater total dissolved P (TDP) could be reproducibly subdivided into 3 chem. distinct pools: sol. reactive P (SRP; presumably dominated by PO43-), UV-labile P (PUV-L; contg. primarily monophosphate esters), and UV-stable P (PUV-S; contg. primarily **nucleotide** di- and triphosphates, nucleic acids, and other compds. resistant to UV treatment). Field application of these procedures to samples collected at Station ALOHA from Sept. 1991 to Mar. 1992 (HOT-30 to HOT-35), showed the presence of all 3 operationally defined pools. In the upper portion of the water column (0-100 m), the TDP pool (29.26 .+-. 2.32 mmol P/m2) contained, on av., 23% SRP, 26% PUV-S, and 51% PUV-L. With increasing depth, the concn. of PUV-L decreased, whereas that of the PUV-S pool increased; the PUV-L:PUV-S ratios decreased from values of 2-5 in the upper water column to .ltoreq.1.0 at 200 m.

L15 ANSWER 12 OF 74 MEDLINE
AN 97183013 MEDLINE
DN 97183013
TI Rapid directional walk within DNA clones by step-out PCR.
AU Wesley U V; Wesley C S
CS Rockefeller University, New York, NY, USA.
SO METHODS IN MOLECULAR BIOLOGY, **(1997)**, 67 279-85.
Journal code: BU3. ISSN: 1064-3745.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199706
EW 19970603

L15 ANSWER 13 OF 74 CAPLUS COPYRIGHT 2000 ACS DUPLICATE 2
AN 1997:641764 CAPLUS
DN 127:327058
TI Palindromic **oligonucleotide**-directed enzymic determination of 2'-**deoxythymidine 5'-triphosphate** and 2'-**deoxycytidine 5'-triphosphate** in human cells
AU Zhang, Hao; Wood, Owen L.; Papermaster, Susan F.; Nielsen, Carl J.; Ussery, Michael A.
CS Antiviral Res. Lab., Div. Antiviral Drug Products (HFD-535), Cent. Drug Evaluation Res., US. FDA, Rockville, MD, 20857, USA
SO Anal. Biochem. (**1997**), 252(1), 143-152
CODEN: ANBCA2; ISSN: 0003-2697
PB Academic

DT Journal
LA English
AB With increasing awareness of the roles of intracellular dNTPs in the replication of HIV and in anti-HIV combination therapy, procedures for the quant. detn. of intracellular dNTPs have assumed great importance. Therefore, a new method is presented for the detn. of the concns. of the 2 title compds. within human cells based on the palindromic **oligonucleotide**-directed enzymic reaction (PODER) using DNA polymerase. Two 19-mer **oligonucleotide** precursors are employed that contain a common 8-mer palindromic sequence followed by a sequence-specific insertion site and a 5'-**oligodeoxythymidylate** tail. To conduct a measurement, 2 mols. of the 19-mer **oligonucleotide** precursor are first annealed to form a pair of sym. template-primer addn. sites at their 3'-termini that are coded for the analyte of interest, present in limiting amts. The Klenow fragment of Escherichia coli DNA polymerase I then elongates template-primer by the addn. of 2 mols. of the complementary deoxyribonucleotide analyte. Following the addn. of the analyte mols., the template-primer is extended with a 10-mer **oligo**(dA) tail in the presence of excess dATP and the Klenow fragment. The result is a 30-mer palindromic **oligonucleotide** that can be sepd. from any remaining 19-mer precursor and quantified by paired-ion HPLC using UV detection. Since the molar extinction coeff. of the 30-mer palindromic **oligonucleotide** is much larger than that of the **nucleotide** analyte alone, the UV signal is markedly enhanced, thereby increasing sensitivity. Details describing this method and the application of it to measure these analytes is as few as 2.5 .times. 106 human cells are presented.

L15 ANSWER 14 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1996:290804 CAPLUS
DN 124:334829
TI Use of deoxyribose nicotinamide adenine dinucleotide to enhance specificity of NAD-dependent ligation reactions
IN Wallace, Robert B.; Juarez-Salinas, Hector; Ugozzoli, Luis
PA Bio-Rad Laboratories, Inc., USA
SO U.S., 18 pp.
CODEN: USXXAM
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 5508179	A	19960416	US 1994-214636	19940318 <--

PI
AB .beta.-2'- Or 3'-deoxyribose NAD are used to enhance specificity of NAD-dependent ligation reactions. This method may be used in such procedures as ligase chain reaction (LCR) and in application of LCR to detection of genetic mutations. Use of .beta.-3'-deoxyribose NAD in an LCR-based detection of sickle cell anemia .beta.S mutation resulted in less template-independent ligation and 20-fold fewer mismatch ligation products.

L15 ANSWER 15 OF 74 MEDLINE
AN 97094960 MEDLINE
DN 97094960
TI Proliferating cell nuclear antigen promotes misincorporation catalyzed by calf thymus DNA polymerase delta.
AU Mozzherin D J; McConnell M; Jasko M V; Krayevsky A A; Tan C K; Downey K M; Fisher P A
CS Department of Pharmacological Sciences, University Medical Center, State

University of New York, Stony Brook, New York 11794-8651, USA..
paul@pharm.s[redacted]sb.edu
NC ES-04068 (NIEHS)
DK-26206 (NIDDK)
SO JOURNAL OF BIOLOGICAL CHEMISTRY, **(1996 Dec 6)** 271 (49) 31711-7.
Journal code: HIV. ISSN: 0021-9258.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 199703
AB A proliferating cell nuclear antigen (PCNA)-dependent complex, detectable after nondenaturing polyacrylamide gel electrophoresis, is formed between calf thymus DNA polymerase delta (pol delta) and synthetic **oligonucleotide** template-primers containing a mispaired **nucleotide** at the 3'-terminal position of the primer. This complex is indistinguishable in composition from that formed with a fully base paired template-primer. Extension of a mispaired primer terminus is a component of DNA polymerase fidelity. The fidelity of pol delta on synthetic **oligonucleotide** template-primers was compared with and without its specific processivity factor, PCNA. In the absence of PCNA, pol delta misincorporates less than one **nucleotide** for every 100,000 **nucleotides** incorporated correctly. Addition of PCNA to reactions reduces fidelity by at least 27-fold. PCNA also confers upon pol delta, the ability to incorporate (and/or not excise) the dTTP analog, 2'-**deoxythymidine**-5'-O-(alpha-phosphonomethyl)-beta, gamma-diphosphate. A model is proposed whereby the increased stability (decreased off-rate) of the pol delta template-primer complex in the presence of PCNA facilitates unfavorable events catalyzed by pol delta. This model suggests an explicit mechanistic requirement for the intrinsic 3'-5'-exonuclease of pol delta.

L15 ANSWER 16 OF 74 MEDLINE
AN 97121256 MEDLINE
DN 97121256
TI Human telomerase inhibition by 7-deaza-2'-deoxypurine nucleoside triphosphates.
AU Fletcher T M; Salazar M; Chen S F
CS Cancer Therapy and Research Center, Institute for Drug Development, San Antonio, Texas 78245, USA.
NC U19 CA 67760 (NCI)
SO BIOCHEMISTRY, **(1996 Dec 10)** 35 (49) 15611-7.
Journal code: A0G. ISSN: 0006-2960.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199703
EW 19970303
AB Telomeres play an important role in chromosome organization and stability.
Human telomerase is a terminal transferase that adds TTAGGG units onto the telomere end. In general, telomerase activity is not detected in normal somatic cells but is present in immortalized cells. Consequently, telomerase might be a selective target for cancer chemotherapy. Using cell-free biochemical telomerase assay, we have found that 7-deaza-2'-**deoxyguanosine-5'-triphosphate** (7-deaza-dGTP) and 7-deaza-2'-**deoxyadenosine-5'-triphosphate** (7-deaza-dATP) were potent telomerase inhibitors. The concentrations of inhibitors in which 50% of the telomerase activity was inhibited (IC50 values) were 11 and 8 microM for 7-deaza-dGTP and 7-deaza-dATP, respectively. Additional studies show that both 7-deaza-dGTP and

7-deaza-dATP were also incorporated into telomeric DNA by telomerase. However, incorporation of 7-deaza-dATP or 7-deaza-dGTP results in a telomeric ladder that is prematurely shortened. No difference in the number or position of pause sites were observed when 7-deaza-dATP was compared to dATP as substrates. On the other hand, both a shift and an increase in pause sites was observed when dGTP was replaced by 7-deaza-dGTP. Incorporation of 7-deaza **nucleotides** by telomerase may be used as a tool for the study of telomerase mechanism and function. In addition, this may be a novel approach in the design of new telomerase inhibitors.

L15 ANSWER 17 OF 74 MEDLINE
AN 96312900 MEDLINE
DN 96312900
TI Steady-state and pre-steady-state kinetic analysis of dNTP insertion opposite 8-oxo-7,8-dihydroguanine by Escherichia coli polymerases I exo- and II exo-.
AU Lowe L G; Guengerich F P
CS Department of Biochemistry, Vanderbilt University School of Medicine, Nashville, Tennessee 37232-0146, USA.
NC CA44353 (NCI)
ES00267 (NIEHS)
ES07028 (NIEHS)
SO BIOCHEMISTRY, **(1996 Jul 30)** 35 (30) 9840-9.
Journal code: A0G. ISSN: 0006-2960.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199611
AB Escherichia coli polymerases (pol) I exo-(KF-) and pol II exo- (pol II-) were used as model enzymes with a DNA primer/template complex (12/16-mer) to examine the kinetics of incorporation of dCTP and dATP at the site of an 8-oxo-7,8-dihydroguanine (8-oxoGua) residue; compared to guanine (Gua).
In steady-state assays (with DNA in excess) the rate of incorporation (kcat) was dCTP > dATP and the K(m),dATP < K(m),dCTP during incorporation opposite 8-oxoGua with both polymerases. Pre-steady-state kinetic curves (rapid-quench analysis) for the addition of C opposite 8-oxoGua or Gua by KF- and pol II- were all biphasic, with a rapid initial single-turnover burst followed by a slower multiple turnover rate, while addition of A opposite 8-oxoGua did not display burst kinetics with either enzyme. Reduced rates of incorporation of the dCTP alpha S and dATP alpha S phosphorothioate analogs suggest that the rates of incorporation of A and C opposite 8-oxoGua are limited during polymerization by the rate of phosphodiester bond formation. Neither polymerase appears to discriminate between adducted and nonadducted DNA substrate for binding. Kinetic assays performed with varying dCTP concentrations indicate that dCTP has a higher K(d) and lower k(p) (polymerization rate) for incorporation opposite 8-oxoGua compared to Gua. Furthermore, the dATP binding affinities with KF- and pol II- were approximately 10- and approximately 3-fold lower, respectively, than that of dCTP as determined in competition assays with mixtures of dCTP and dATP. Microscopic rate constants were estimated by mathematical analysis of dNTP concentration dependence curves. Both polymerases preferentially extended the A:8-oxoGua pair while extension of the C:8-oxoGua pair was greatly impaired. Based on these findings, the fidelity of KF- and pol II- during replication of 8-oxoGua depends on contributions from **nucleotide** binding, the rate of phosphodiester bond formation, and the ease of base pair extension.

L15 ANSWER 18 OF 74 MEDLINE
AN 96214911 MEDLINE

DN 96214911
TI Human immunodeficiency virus reverse transcriptase. Functional mutants obtained by random mutagenesis coupled with genetic selection in Escherichia coli.
AU Kim B; Hathaway T R; Loeb L A
CS Joseph Gottstein Memorial Cancer Research Laboratory, Department of Pathology, Box 357705, University of Washington, Seattle, Washington 98195-7705, USA.
NC R35-CA-39903 (NCI)
5T32-CA-09437-13 (NCI)
SO JOURNAL OF BIOLOGICAL CHEMISTRY, **(1996 Mar 1)** 271 (9) 4872-8.
Journal code: HIV. ISSN: 0021-9258.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 199608
AB We describe catalytically active mutants of HIV RT (human immunodeficiency virus reverse transcriptase) generated by random sequence mutagenesis and selected in Escherichia coli for ability to complement the temperature-sensitive phenotype of a DNA polymerase I (Pol Its) mutant. We targeted amino acids Asp-67 through Arg-78 in HIV RT, which form part of the beta3-beta4 flexible loop and harbor many of the currently known mutations that confer resistance to nucleoside analogs. DNA sequencing of 109 selected mutants that complement the Pol Its phenotype revealed substitutions at all 12 residues targeted, indicating that none of the wild-type amino acids is essential. However, single mutations were not observed at Trp-71, Arg-72, and Arg-78, consistent with evolutionary conservation of these residues among viral RTs and lack of variation at these positions among isolates from patients. The mutations we recovered included most of those associated with drug resistance as well as previously unidentified mutations. Purification and assay of 14 mutant proteins revealed correlation between their DNA-dependent DNA polymerize activity in vitro and ability to complement the Pol Its phenotype. Activity of several mutants was resistant to 3'-azidothymidine triphosphate. We conclude that random sequence mutagenesis coupled with positive genetic selection in E. coli yields large numbers of functional HIV RT mutants. Among these are less active variants which are unlikely to be isolated from HIV-infected individuals and which will be informative of the roles of individual amino acids in the catalytic functions of the enzyme.

L15 ANSWER 19 OF 74 MEDLINE
AN 96183916 MEDLINE
DN 96183916
TI Studies of neutralizing monoclonal antibody to human immunodeficiency virus type 1 reverse transcriptase: antagonistic and synergistic effects in reactions performed in the presence of nucleoside and nonnucleoside inhibitors, respectively.
AU Gu Z; Li X; Quan Y; Parniak M A; Wainberg M A
CS McGill University AIDS Centre, McGill University, Montreal, Quebec, Canada.
SO JOURNAL OF VIROLOGY, **(1996 Apr)** 70 (4) 2620-6.
Journal code: KCV. ISSN: 0022-538X.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 199609
AB We have assessed interactions between the reverse transcriptase (RT) of human immunodeficiency virus type 1 (HIV-1) and a neutralizing monoclonal

antibody (1E8) that hinders binding of deoxynucleoside triphosphate (dNTP)
substrates. Steady-state reactions with homopolymeric template-primers revealed that 1E8 antagonized inhibition of RT activity mediated by 3'-azido-3'-**deoxythymidine** triphosphate and 2',3'-dideoxycytidine triphosphate. However, an additive or synergistic inhibition of RT polymerase activity was noted when 1E8 and the nonnucleoside RT inhibitors nevirapine and delavirdine were studied. Chain
elongation and dNTP incorporation studies using an HIV-1 genome-derived heteropolymeric template and either **oligodeoxynucleotide** or tRNA3(Lys) as the primer yielded results consistent with the above observations. 1E8 also increased pausing at certain sites during synthesis
of negative-strand, strong-stop DNA, whether or not ddNTP and nonnucleoside RT inhibitors were present.

L15 ANSWER 20 OF 74 CAPLUS COPYRIGHT 2000 ACS DUPLICATE 3
AN 1996:79343 CAPLUS
DN 124:110707
TI Cooperative Interactions of **Nucleotide** Ligands Are Linked to **Oligomerization** and DNA Binding in Bacteriophage T7 Gene 4 Helicases
AU Hingorani, Manju M.; Patel, Smita S.
CS Department of Biochemistry, Ohio State University, Columbus, CO, 43210, USA
SO Biochemistry (**1996**), 35(7), 2218-28
CODEN: BICHAW; ISSN: 0006-2960
DT Journal
LA English
AB The equil. **nucleotide** binding and **oligomerization** of bacteriophage T7 gene 4 helicases have been investigated using thymidine **5'-triphosphate** (dTTP), **deoxythymidine**.
5'-(.beta.,.gamma.-methylenetriphosphate) (dTMP-PCP), thymidine 5'-diphosphate (dTDP), ATP, and adenosine 5'-O-(3-thiotriphosphate) (ATP.gamma.S). In the presence of **nucleotide** ligands, T7 helicases self-assemble into hexamers with six potential **nucleotide** binding sites that are nonequivalent both in the absence and in the presence of single-stranded DNA. All **nucleotides** tested bind with high affinity to three sites (Kd = 5.times.10-6 M, dTTP; 6.times.10-7 M, dTMP-PCP; 4.times.10-6 M, dTDP; 3.times.10-5 M, ATP; 2.times.10-6 M, ATP.gamma.S), while binding to the remaining sites is undetectable. Interestingly, **nucleotide** binding to the high-affinity sites exhibits pos. cooperativity which is sensitive to protein concn. This effect is a result of ligand binding-linked **oligomerization** wherein helicase **oligomer** equil. changes as a function of both **nucleotide** and protein concn. A study of DNA binding shows that 1-2 NTPs bound per hexamer are sufficient for stoichiometric interaction between the helicase and DNA. Thus, the ring-shaped helicase hexamers assemble around DNA with one, two,
or three NTPs bound to each hexamer. This study also examines the preferred use of dTTP for T7 helicase-catalyzed DNA unwinding by comparison with ATP, the more commonly used **nucleotide** ligand. ATP binds to the helicase with 6-fold weaker affinity than dTTP and promotes hexamerization as well as DNA binding. Nevertheless, DNA unwinding with ATP is at least 100-fold slower than with dTTP. Thus, the difference in ATP and dTTP utilization probably lies in a highly specific step in the coupling of NTP hydrolysis to DNA unwinding.

L15 ANSWER 21 OF 74 MEDLINE
AN 97123975 MEDLINE
DN 97123975
TI Functional characterization of the genes coding for the terminal protein and DNA polymerase from bacteriophage GA-1. Evidence for a sliding-back

mechanism du[redacted] protein-primed GA-1 DNA repli[redacted]tion.
AU Illana B; Bla[redacted]o L; Salas M
CS Centro de Biologia Molecular Severo Ochoa (CSIC-UAM), Universidad Autonoma, Madrid, Spain.
NC 5RO1 GM 27242-16 (NIGMS)
SO JOURNAL OF MOLECULAR BIOLOGY, **(1996 Dec 6)** 264 (3) 453-64.
Journal code: J6V. ISSN: 0022-2836.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
OS GENBANK-X96987
EM 199703
AB We have determined the **nucleotide** sequence of 2676 bp at the left part of the linear genome of Bacillus subtilis bacteriophage GA-1. Computer analysis revealed that this fragment contains two open reading frames (ORFs), ORF1 and ORF2, which contain 265 and 578 codons, respectively. Data base search revealed that ORF1 and ORF2 might encode proteins similar to the terminal protein (TP) and DNA polymerase, respectively, of bacteriophage phi29. By using extracts of B. subtilis infected with GA-1, we demonstrated that GA-1 DNA replication occurs by a protein-priming mechanism in which these two viral proteins are involved. Butylphenyl dGTP (BuPdGTP), a specific inhibitor of eukaryotic-type (family B) DNA polymerases, inhibited both the protein-primed initiation step and DNA polymerization during GA-1 DNA replication. These results suggest the involvement of a eukaryotic-type DNA polymerase, probably the product of the viral ORF2, in both stages of a replication process in which the TP primes replication at both DNA ends (replication origins). Using synthetic **oligonucleotides**, we carried out a mutational analysis of the GA-1 DNA right end to determine the initiation site for replication. The results indicate that initiation of replication mainly occurs opposite the second **nucleotide** at the 3' end of the template, although the third **nucleotide** can be used as an alternative initiation site. As in other TP-containing genomes, a sliding-back mechanism is proposed to account for the maintenance of the DNA length at the GA-1 DNA ends.

L15 ANSWER 22 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1996:734689 CAPLUS
DN 126:15242
TI Matrix-assisted laser desorption/ionization time-of-flight mass spectrometry for the detection of polymerase chain reaction products containing 7-deazapurine moieties
AU Siegert, C. W.; Jacob, A.; Koester, H.
CS Faculty of Chemistry, University of Hamburg, Hamburg, D-20146, Germany
SO Anal. Biochem. **(1996)**, 243(1), 55-65
CODEN: ANBCA2; ISSN: 0003-2697
PB Academic
DT Journal
LA English
AB Double-stranded DNA fragments of different length with and without the incorporation of 7-deazapurine deoxynucleotides have been prepd. via the polymerase chain reaction (PCR) using exo(-) Pyrococcus furiosus DNA polymerase, unmodified primers, and c7-dATP and c7-dGTP as the only purine triphosphates. In spite of the presence of some unmodified purine moieties due to the primers, matrix-assisted laser desorption/ionization time-of-flight (MALDI-TOF) mass spectrometry revealed remarkable differences between the modified and unmodified DNA fragments. The incorporation of 7-deazapurine **nucleotides** resulted in a significant redn. of fragmentation and therefore in increased signal intensities and higher mass resoln. The mol. wts. could be detd. with an accuracy of up to 0.03%. Mass resoln. was sufficient to resolve the (M + H)+ signals of the two single strands of a 7-deazapurine-contg. 99-base-pair DNA duplex. Thus, MALDI-OF mass spectrometry offers a very

fast and acc[redacted]e way to detect and analyze s[redacted] PCR products sufficient in length for many diagnostic applications wi[redacted]ut gel electrophoresis
and
labeling.

L15 ANSWER 23 OF 74 MEDLINE
AN 96104554 MEDLINE
DN 96104554
TI Effects of reverse transcriptase inhibitors on telomere length and telomerase activity in two immortalized human cell lines.
AU Strahl C; Blackburn E H
CS Department of Microbiology and Immunology, University of California, San Francisco 94143-0414, USA.
NC GM26259 (NIGMS)
SO MOLECULAR AND CELLULAR BIOLOGY, **(1996 Jan)** 16 (1) 53-65.
Journal code: NGY. ISSN: 0270-7306.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199603
AB The ribonucleoprotein telomerase, a specialized cellular reverse transcriptase, synthesizes one strand of the telomeric DNA of eukaryotes. We analyzed telomere maintenance in two immortalized human cell lines:
the
B-cell line JY616 and the T-cell line Jurkat E6-1, and determined whether known inhibitors of retroviral reverse transcriptases could perturb telomere lengths and growth rates of these cells in culture. Dideoxyguanosine (ddG) caused reproducible, progressive telomere shortening over several weeks of passaging, after which the telomeres stabilized and remained short. However, the prolonged passaging in ddG caused no observable effects on cell population doubling rates or morphology. Azidothymidine (AZT) caused progressive telomere shortening
in
some but not all T- and B-cell cultures. Telomerase activity was present in both cell lines and was inhibited in vitro by ddGTP and AZT triphosphate. Prolonged passaging in arabinofuranyl-guanosine, dideoxyinosine (ddI), dideoxyadenosine (ddA), didehydrothymidine (d4T),
or
phosphonoformic acid (foscarnet) did not cause reproducible telomere shortening or decreased cell growth rates or viabilities. Combining AZT, foscarnet, and/or arabinofuranyl-guanosine with ddG did not significantly augment the effects of ddG alone. Strikingly, with or without inhibitors, telomere lengths were often highly unstable in both cell lines and varied between parallel cell cultures. We propose that telomere lengths in these T- and B-cell lines are determined by both telomerase and telomerase-independent mechanisms.

L15 ANSWER 24 OF 74 MEDLINE
AN 96209928 MEDLINE
DN 96209928
TI Single-step purification of recombinant wild-type and mutant HIV-1 reverse
transcriptase.
AU Fletcher R S; Holleschak G; Nagy E; Arion D; Borkow G; Gu Z; Wainberg M A;
Parniak M A
CS Lady Davis Institute for Medical Research, Sir Mortimer B. Davis- Jewish General Hospital, Montreal, Canada.
SO PROTEIN EXPRESSION AND PURIFICATION, **(1996 Feb)** 7 (1) 27-32.
Journal code: BJV. ISSN: 1046-5928.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals

EM 199708
AB We have devis[illegible] a single-step method that enab[illegible]s purification of HIV-1 recombinant reverse transcriptase directly from bacterial lysates in less than 2 h. Clarified lysates are applied to commercial Q- and S-matrix cartridge columns connected in series. The columns are washed with low-salt buffer to remove unbound protein, then the Q column is removed and reverse transcriptase is eluted from the S column using a salt gradient. The purification has been carried out with both medium-pressure and high-pressure chromatographic systems. Purifications are carried out at room temperature near neutral pH, providing enzyme with high DNA polymerase specific activity. A crucial aspect of the procedure is the use of Tris buffer, a buffer that is normally incompatible in cation-exchange methods. The method is applicable for the purification of the p51/p66 heterodimer and the p51 and p66 homodimer forms of reverse transcriptase. We have used this method to purify wild-type reverse transcriptase and several recombinant proteins containing mutations correlated with dideoxynucleoside drug resistance.

L15 ANSWER 25 OF 74 MEDLINE
AN 96125081 MEDLINE
DN 96125081
TI Effects of non-nucleoside inhibitors of human immunodeficiency virus type 1 in cell-free recombinant reverse transcriptase assays.
AU Gu Z; Quan Y; Li Z; Arts E J; Wainberg M A
CS McGill University AIDS Centre, Lady Davis Institute-Jewish General Hospital, Montreal, Quebec, Canada.
SO JOURNAL OF BIOLOGICAL CHEMISTRY, **(1995 Dec 29)** 270 (52) 31046-51.
Journal code: HIV. ISSN: 0021-9258.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 199604
AB We have employed a cell-free human immunodeficiency virus type 1 (HIV-1) reverse transcriptase (RT) assay to study the effects of non-nucleoside inhibitors of RT (NNRTI) by directly monitoring specific HIV DNA products using a HIV-1 genome-derived template and an **oligodeoxynucleotide** primer. As previously shown by ourselves and others, nucleoside analog triphosphates, e.g. 3'-azido-3'-**deoxythymidine** triphosphate and 2',3'-dideoxyadenosine triphosphate, could directly inhibit HIV RT RNA-dependent DNA polymerase activity by causing chain termination, as visualized in a RT reaction that yields specific DNA products. In contrast, each of two NNRTIs, nevirapine and delavirdine, directly inhibited RT activity without causing chain termination effects. We also analyzed interactions between nucleoside analogs and NNRTIs or among NNRTIs by chain elongation/dNTP incorporation and/or steady-state kinetic assays. Combinations of nevirapine with the triphosphates of either the (-)-strand of 2',3'-dideoxy-3'-thiacytidine or 2',3'-dideoxyadenosine yielded additive/synergistic effects on RT activity. However, only an additive effect was observed when combinations of nevirapine and 3'-azido-3'-**deoxythymidine** triphosphate were employed. Combinations of nevirapine and delavirdine had an antagonistic effect on the inhibition of HIV-1 RT activity.

L15 ANSWER 26 OF 74 MEDLINE
AN 95370204 MEDLINE
DN 95370204
TI Efficient incorporation of anti-HIV deoxynucleotides by recombinant yeast mitochondrial DNA polymerase.
AU Eriksson S; Xu B; Clayton D A
CS Department of Developmental Biology, Stanford University School of Medicine, California 94305-5427, USA.
NC GM33088-23 (NIGMS)

SO JOURNAL OF B[redacted]OGICAL CHEMISTRY, **(1995 Aug 11)** [redacted]70 (32) 18929-34.
Journal code: HIV. ISSN: 0021-9258.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 199511
AB Saccharomyces cerevisiae mtDNA polymerase, isolated as a single 135-kDa recombinant polypeptide, showed high processivity and a capacity of use poly(dA).**oligo**(dT), poly(rA).**oligo**(dT), or primed bacteriophage M13 DNA as a template. In a primer extension assay, the enzyme exhibited an intrinsic 3'-5'-exonuclease activity. By optimizing the polymerization reaction conditions, apparent Km and Vmax values could be determined for the incorporation of dTTP, 2'-3'-dideoxy-TTP (ddTTP), 3'-azido-TTP (AZTTP), 3'-fluoro-TTP, dCTP, 2'-3'-dideoxy-CTP, and didehydro(d4)CTP. The yeast mtDNA polymerase used ddTTP, 3'-fluoro-TTP, and ddCTP almost as efficiently as natural deoxynucleoside trisphosphates.
Both 3'AZTTP and d4CTP were each significantly less efficient as substrates. Overall, the kinetic data with mtDNA polymerase were very similar to those of the recombinant human immunodeficiency virus reverse transcriptase control. Terminally incorporated AZTTP or ddTTP was not removed by the 3'-5' exonuclease activity of mtDNA polymerase. This may explain the inhibition of mtDNA replication observed in anti-human immunodeficiency virus treatment with dideoxynucleoside analogs for their effects of mtDNA polymerase could be of value in future rational drug design.

L15 ANSWER 27 OF 74 MEDLINE
AN 96101441 MEDLINE
DN 96101441
TI Primer synthesis kinetics by Escherichia coli primase on single-stranded DNA templates.
AU Swart J R; Griep M A
CS Department of Chemistry, University of Nebraska, Lincoln 68588-0304, USA.
NC GM 47490 (NIGMS)
SO BIOCHEMISTRY, **(1995 Dec 12)** 34 (49) 16097-106.
Journal code: A0G. ISSN: 0006-2960.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199603
AB The kinetics of primer RNA initiation and elongation by Escherichia coli primase were measured. The single-stranded DNA template that was used to develop the system, d(CAGA-(CA)5CTGCAAAGC), contained: (1) the preferred initiating trinucleotide d(CTG); (2) five residues 3' to the d(CTG), the minimum required for efficient primer synthesis; and (3) a single guanine placed near the 5'-end to facilitate study of cytidine triphosphate analog incorporation at a unique site. The assay monitored radiolabeled **nucleotide** incorporation into the RNA primers. The various primers were separated by length using denaturing polyacrylamide gel electrophoresis. Different types of primers were observed when synthesis was monitored using gamma- versus alpha-radiolabeled **nucleotides** as the probe. When [gamma-32P]-ATP incorporation was the probe, only primers initiated with ATP from the unique template thymine were observed.
The sequences of these primers were complementary to that of the template.
No primers shorter than a 12-mer accumulated, demonstrating that formation of the first phosphodiester bond was much slower than that of the next 10

phosphodiest[illegible]onds. The longest primer obse[illegible]d when monitoring [gamma-32P]ATP incorporation was 16 **nucleotide**s long, the correct length for a primer completely template-directed and initiated at the unique thymine. Misinsertion of a noncognate **nucleotide** at the template's guanine indicated very poor **nucleotide** discrimination by this enzyme. When [alpha-32P]UTP was the probe for primer synthesis, all primers synthesized were observed whether or not they were initiated with ATP. Under these conditions, "overlong" primers and the above-described template length-dependent primers were observed. The template length-dependent primers accumulated faster than the overlong primers, but, at long incubation times, the overlong primers became the dominant species. The overlong primers were not fully related to the template length-dependent primers since they were not initiated complementary to the template d(CTG)n. Nevertheless, the overlong primers did appear to arise as a consequence of the template length-dependent species since their length was double and they arose in the time course after the length-dependent species.

L15 ANSWER 28 OF 74 CAPLUS COPYRIGHT 2000 ACS DUPLICATE 4
AN 1995:531370 CAPLUS
DN 123:78025
TI Human immunodeficiency virus type 1 reverse transcriptase. 3'-Azidodeoxythymidine **5'-triphosphate** inhibition indicates two-step binding for template-primer
AU Jaju, Madhuri; Beard, William A.; Wilson, Samuel H.
CS Sealy Center Molecular Science, University Texas Medical Branch, Galveston, TX, 77555-1068, USA
SO J. Biol. Chem. (**1995**), 270(17), 9740-7
CODEN: JBCHA3; ISSN: 0021-9258
DT Journal
LA English
AB Human immunodeficiency virus type-1 (HIV-1) reverse transcriptase (RT) catalyzes DNA synthesis by an ordered sequential mechanism. After template-primer (T.cntdot.P) binds to free enzyme, the deoxynucleoside triphosphate to be incorporated binds to the RT and T.cntdot.P binary complex (RTT.cntdot.P). After incorporation of the bound **nucleotide**, catalytic cycling is limited either by a conformational change (for processive synthesis) or release of the enzyme from the extended T.cntdot.P (for single-**nucleotide** incorporation). To explore cycling through these alternate rate-limiting steps, we detd. kinetic parameters for single-**nucleotide** incorporation by HXB2R HIV-1 RT with chain-terminating **nucleotide** substrates 3'-azido-3'-**deoxythymidine** triphosphate (AZTTP) and dideoxythymidine triphosphate on a homopolymeric T.cntdot.P system, poly(rA)-**oligo**(dT)16. Inhibition of processive **deoxythymidine** monophosphate incorporation by these chain-terminating substrates was also examd. Because AZTTP is a substrate, its Km should be equiv. to Ki, and since Km for AZTTP should be influenced by the dissocn. rate const. for RTT.cntdot.P, we examd. the effect of altering RTT.cntdot.P dissocn. on AZTTP kinetic parameters. The dissocn. rate const. was modulated by making use of different T.cntdot.P substrates, viral sources of RT, and a mutant RT altered at a residue that perturbs T.cntdot.P binding. As expected from earlier work, the time course of AZTMP incorporation on poly(rA)-**oligo**(dT)16 was biphasic, with a burst followed by a slower steady-state phase representing kcat (0.42 min-1) which was similar to the rate const. for RTT.cntdot.P dissocn. Addnl., Km for AZTTP (110 nM) was lower than its equil. dissocn. const. (1200 nM). AZTTP inhibition (Ki,AZTTP) of processive dTMP incorporation and incorporation of a single **nucleotide** were similar. However, a simple correlation between the RTT.cntdot.P dissocn. rate const. and Ki,AZTTP was not obsd. These

results indi[redacted]e that a simple ordered model [redacted] single-**nucleotide** incorporation is inadequate and that different forms of RTT.cntdot.P exist which can limit catalysis. The results are discussed in the context of a two-step binding reaction for T.cntdot.P where the binary RTT.cntdot.P complex undergoes an isomerization before binding of the deoxynucleotide substrate.

L15 ANSWER 29 OF 74 CAPLUS COPYRIGHT 2000 ACS DUPLICATE 5
AN 1995:479837 CAPLUS
DN 122:281530
TI Mutated K65R recombinant reverse transcriptase of human immunodeficiency virus type 1 shows diminished chain termination in the presence of 2',3'-dideoxycytidine **5'-triphosphate** and other drugs
AU Gu, Zhengxian; Arts, Eric J.; Parniak, Michael A.; Wainberg, Mark A.
CS Lady Davis Institute-Jewish General Hospital, McGill University AIDS Center, Montreal, PQ, H3T 1E2, Can.
SO Proc. Natl. Acad. Sci. U. S. A. (**1995**), 92(7), 2760-4
CODEN: PNASA6; ISSN: 0027-8424
DT Journal
LA English
AB A lysine-to-arginine substitution at amino acid 65 (K65R) in human immunodeficiency virus type 1 (HIV-1) reverse transcriptase (RT) is assocd. with resistance to 2',3'-dideoxycytidine (ddC), 2',3'-dideoxyinosine (ddI), and the (+) enantiomer of 2',3'-dideoxy-3'-thiacytidine (3TC). To further characterize the mol. basis of such resistance, we expressed the p66/p51 heterodimer of wild-type RT, K65R mutated RT, and a doubly mutated (K65R/M184V) RT in Escherichia coli and assessed the characteristics of **nucleotide** incorporation and chain termination in cell-free reverse transcription reactions in the presence and absence of various nucleoside triphosphate analogs. These reactions employed a HIV RNA template (HIV-PBS) that contained the primer binding sequence (PBS) and the U5 and R regions of HIV-1 genomic RNA and an **oligodeoxynucleotide** (dPR) complementary to the HIV-1 PBS as primer. The K65R and K65R/M184V RTs showed significantly decreased chain-termination effects during polymn. with the **5'-triphosphates** of ddC, 3TC, 2',3'-dideoxyadenosine, and AZT (3'-azido-3'-**deoxythymidine**) in comparison with wild-type RT. Detailed anal. with ddCTP and wild-type RT revealed that chain termination occurred at all guanines in the RNA template. However, the frequency of dideoxynucleoside triphosphate (ddNTP)-induced chain termination was decreased at certain guanines but not others in reactions catalyzed by K65R RT. Both the K65R mutant RT and wild-type RT had similar processive activity. These results indicate that decreased chain termination of K65R RT in the presence of ddNTPs is consistent with data obtained in viral replication assays.

L15 ANSWER 30 OF 74 MEDLINE
AN 95246240 MEDLINE
DN 95246240
TI DNA polymerase action on an **oligonucleotide** containing a site-specifically located N-(deoxyguanosin-8-yl)-1-aminopyrene.
AU Vyas R R; Basu A K
CS Department of Chemistry, University of Connecticut, Storrs 06269, USA.
NC ES05695 (NIEHS)
SO CARCINOGENESIS, **(1995 Apr)** 16 (4) 811-6.
Journal code: C9T. ISSN: 0143-3334.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 199508
AB A 25mer **oligonucleotide** containing a single N-(deoxyguanosin-8-

yl-)-1-aminopyrene (dGAP), the major DNA adduct formed by reductively activated 1-[redacted]ropyrene, was synthesized. The [redacted]duct was located at **nucleotide** 21 from the 3' end. DNA synthesis on this template by human DNA polymerases alpha and beta, HIV reverse transcriptase, Sequenase (version 2.0) and Klenow fragment of DNA polymerase I was strongly blocked at the **nucleotide** 3' to the adduct site. Only when a 3'-->5' exonuclease-deficient Klenow fragment was used was incorporation of a **nucleotide** opposite the adduct observed. Nevertheless, extension beyond the adduct site did not occur to a significant extent. Only a relatively small proportion of full-length product (< 5%) was detected. In the presence of Mn2+, the efficiency of bypass with this polymerase increased. When a 20mer primer was elongated in the presence of only one **nucleotide** triphosphate, deoxycytidylic acid was preferentially incorporated opposite the adduct. **Deoxycytidine** opposite the adduct was also preferred when a set of 21mer primers (containing each of the four **nucleotides** opposite dGAP) were elongated to a full-length product in the presence of all four deoxynucleotide triphosphates. In order to confirm these results, extension of a 15mer primer was carried out with all four deoxynucleotide triphosphates and the products were isolated. Maxam--Gilbert sequencing of each elongation product showed that primer extension occurred in an error-free manner. We conclude that dGAP is a strong block of DNA replication. However, when translesion synthesis occurs, it is largely accurate.

L15 ANSWER 31 OF 74 CAPLUS COPYRIGHT 2000 ACS DUPLICATE 6
AN 1995:622112 CAPLUS
DN 123:136902
TI New **nucleotide** inhibitors of human DNA polymerase .alpha.
AU Semizarov. D. G.; Jasko, M. V.; Kukhanova, M. K.; Krayevsky, A. A.
CS Engelhardt Inst. Mol. Biol., Russian Acad. Sci., Moscow, 117984, Russia
SO Mol. Biol. (Moscow) (**1995**), 29(3), 689-700
CODEN: MOBIBO; ISSN: 0026-8984
DT Journal
LA Russian
AB 2'-**Deoxythymidine 5'-triphosphate** and 2'-**deoxyadenosine 5'-triphosphate** analogs contg. a methylene group between the .alpha. phosphorus and 5' oxygen were synthesized. The substrate properties of these compds. toward some mammalian DNA polymerases and retroviral reverse transcriptases were evaluated using a system contg. phage M13mp10 DNA, a synthetic **oligonucleotide**, and the enzyme. The compds. contg. a hydroxyl at the 3' position were incorporated into the DNA chain by DNA polymerase .alpha. and terminal deoxynucleotidyltransferase, but were not recognized by retroviral reverse transcriptases and mammalian DNA polymerases .epsilon. and .beta.. The selectivity of the compds. synthesized was capitalized on during simultaneous isolation of DNA polymerases .alpha. and .epsilon. from human placenta. A methylene group was also introduced into the acyclovir mol. It was shown that this modification inactivates furanose-related **nucleotide** analogs, but has a minor effect on the substrate properties of acyclic **nucleotide** analogs.

L15 ANSWER 32 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1995:792430 CAPLUS
DN 123:307442
TI Use of vaccinia virus poly(A) polymerase for RNA 3'-end labeling with a chain-terminating **nucleotide** or a short 3' homopolymer tract
AU Thomson, James G.; Gershon, Paul D.
CS Institute Biosciences and Technology, Texas A & M University, Houston, TX, USA
SO BioTechniques (**1995**), 19(3), 416, 418, 420, 422, 424-5

CODEN: BTNQDC ISSN: 0736-6205
DT Journal
LA English
AB Conditions are described for the 3'-end labeling of RNA with 32P 3'-dATP (3'-**deoxyadenosine-5'-triphosphate**), a chain-terminating **nucleotide**, using the poly(A) polymerase (PAP) encoded by vaccinia virus. Reaction time, divalent cation species and concn., and the requirement for both subunits of the PAP were investigated. In the presence of Mn2+, vaccinia PAP is able to tail RNA primers with tracts of 3'-**oligo**(U), **oligo**(C) and **oligo**(G). Conditions for the addn. of labeled 3'-homopolymer tracts were characterized. The use of low **nucleotide** concns. in this study revealed an apparently fixed divalent cation concn. optimum of 0.1 mM, distinct from the previously noted requirement for a 1:1 divalent cation:NTP complex. This indicates a possible requirement for multiple divalent cations in **nucleotidyl** transfer by vaccinia PAP.

L15 ANSWER 33 OF 74 MEDLINE
AN 96063870 MEDLINE
DN 96063870
TI Use of vaccinia virus poly(A) polymerase for RNA 3'-end labeling with a chain-terminating **nucleotide** or a short 3' homopolymer tract.
AU Thomson J G; Gershon P D
CS Institute of Biosciences and Technology, Texas A&M University, Houston, USA.
SO BIOTECHNIQUES, **(1995 Sep)** 19 (3) 416-20, 422-5.
Journal code: AN3. ISSN: 0736-6205.
CY United States
DT Report; (TECHNICAL REPORT)
LA English
FS Priority Journals
EM 199603
AB Conditions are described for the 3'-end labeling of RNA with 32P 3'-dATP (3'-**deoxyadenosine-5'-triphosphate**), a chain-terminating **nucleotide**, using the poly(A) polymerase (PAP) encoded by vaccinia virus. Reaction time, divalent cation species and concentration, and the requirement for both subunits of the PAP were investigated. In the presence of Mn2+, vaccinia PAP is able to tail RNA primers with tracts of 3'-**oligo**(U), **oligo**(C) and **oligo**(G). Conditions for the addition of labeled 3'-homopolymer tracts were characterized. The use of low **nucleotide** concentrations in this study revealed an apparently fixed divalent cation concentration optimum of 0.1 mM, distinct from the previously noted requirement for a 1:1 divalent cation:NTP complex. This indicates a possible requirement for multiple divalent cations in **nucleotidyl** transfer by vaccinia PAP.

L15 ANSWER 34 OF 74 MEDLINE
AN 96007140 MEDLINE
DN 96007140
TI Apoptosis in lactating and involuting mouse mammary tissue demonstrated by nick-end DNA labelling.
AU Quarrie L H; Addey C V; Wilde C J
CS Hannah Research Institute, UK..
SO CELL AND TISSUE RESEARCH, **(1995 Sep)** 281 (3) 413-9.
Journal code: CQD. ISSN: 0302-766X.
CY GERMANY: Germany, Federal Republic of
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199601
AB Mammary involution after cessation of milk removal is associated with extensive loss of secretory epithelial cells. Ultrastructural changes and the appearance of **oligonucleosomal** DNA laddering in ethidium

bromide-stai[redacted] gels indicates that cell loss[redacted]ring involution occurs by apoptosis. In this study, a technique for nick[redacted]nd-labelling of genomic DNA with radiolabelled deoxynucleotide has been used to monitor the induction of programmed cell death in mice after litter removal at peak lactation. This technique proved more sensitive than conventional ethidium bromide staining, and results suggested that apoptosis was induced rapidly by milk stasis, before extensive tissue re-modelling had begun. **Oligonucleosomal** DNA laddering on agarose gels was detected within 24 h of milk stasis, and increased progressively for at least 4 days. Nick-end labelling also detected laddering before litter removal, suggesting that programmed cell death is a normal feature of the lactating tissue. The DNA end-labelling technique was also adapted for in situ visualisation of apoptotic cells in tissue sections. By this criterion, apoptotic cells were identified in both the secretory epithelium lining the alveoli of the gland and, increasingly with prolonged milk stasis, amongst those sloughed into the alveolar lumen. The results demonstrate the utility of these techniques for study of mammary cell death and suggest that, whilst apoptosis is rapidly induced by milk stasis, it is also a normal physiological event in the lactating mammary gland.

L15 ANSWER 35 OF 74 MEDLINE
AN 95306665 MEDLINE
DN 95306665
TI **Nucleotide** binding studies of bacteriophage T7 DNA helicase-primase protein.
AU Patel S S; Hingorani M M
CS Department of Biochemistry, Ohio State University, Columbus 43210, USA.
SO BIOPHYSICAL JOURNAL, **(1995 Apr)** 68 (4 Suppl) 186S-189S; discussion 189S-190S.
Journal code: A5S. ISSN: 0006-3495.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199509
AB Bacteriophage T7 DNA helicase protein is a hexameric protein that contains identical subunits arranged in a ring-like structure. Single-stranded DNA binds through the hole of the ring, and the helicase protein translocates and unwinds duplex DNA using nucleoside triphosphate (NTP) hydrolysis. In our efforts to understand how NTP hydrolysis may be coupled to movement of the helicase on the DNA, we have quantitated the equilibrium binding of **deoxythymidine** triphosphate and thymidine 5'-(beta,gamma-methylenetriphosphate) using nitrocellulose binding assays. Even though the helicase consists of six identical subunits, each hexamer was found to bind only three NTP molecules. These results indicate half-site binding or negative cooperativity in NTP binding by the hexamer. Interestingly, binding of three NTP molecules to the hexamer was sufficient for stoichiometric binding of a single-stranded **oligodeoxynucleotide**. Similar negative cooperativity in NTP binding has also been observed for other helicases, suggesting that it may be a general feature of hexameric helicases. The significance of half-site binding, however, is not understood at the present time.

L15 ANSWER 36 OF 74 MEDLINE
AN 95297704 MEDLINE
DN 95297704
TI Fluorometric measurement of reverse transcriptase activity with

4',6-diamidino-2-phenylindole.

AU Chavan S J; [redacted]chaska H J
CS Molecular Pharmacology and Therapeutics Program, Memorial Sloan-Kettering Cancer Center, New York, New York 10021, USA.
NC NCI-P30-CA-08748 (NCI)
SO ANALYTICAL BIOCHEMISTRY, **(1995 Feb 10)** 225 (1) 54-9.
Journal code: 4NK. ISSN: 0003-2697.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199509
AB We describe a rapid fluorometric assay for reverse transcriptase (RT) activity. After RT is incubated in the presence of poly(A).**oligo** (dT) and dTTP for up to 1 h, the reaction is stopped with EDTA and aliquots are added to cuvettes containing 4',6-diamidino-2-phenylindole (DAPI). DAPI fluorescence, which is increased upon binding the RNA.DNA heteroduplex, is measured after 30 min and is linearly dependent on the enzymatic reaction time and the amount of active RT added to the enzyme assay. The increased fluorescence correlates well with the incorporation of [alpha-32P]dTTP into DNA (r2 = 0.986). However, similar assays with the Klenow fragment using poly(dA).**oligo**(dT) did not result in increased fluorescence under conditions wherein incorporation of [alpha-32P]dTTP into DNA was documented. Thus, the poly(A).poly(dT) [RNA.DNA] heteroduplex must differ from the poly(dA).poly(dT) [DNA.DNA] duplex in a manner that allows for a perturbation of DAPI fluorescence. The relative specific activities of RT in crude preparations measured with the fluorometric assay were comparable to conventional isotopic enzyme assays as were determinations for the type of inhibition and the kinetic constants of purified RT with inhibitors such as zidovudine **5'-triphosphate**, nevirapine, and oltipraz. (ABSTRACT TRUNCATED AT 250 WORDS)

L15 ANSWER 37 OF 74 MEDLINE
AN 95320877 MEDLINE
DN 95320877
TI Reaction between metabolically activated acetaminophen and phosphorothioate **oligonucleotides**.
AU Copple B L; Gmeiner W M; Iversen P L
CS Department of Pharmacology, University of Nebraska Medical Center, Omaha 68198-6260, USA.
SO TOXICOLOGY AND APPLIED PHARMACOLOGY, **(1995 Jul)** 133 (1) 53-63.
Journal code: VWO. ISSN: 0041-008X.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 199510
AB Assessment of toxic or mutagenic risks associated with phosphorothioate **oligonucleotides** (PTO) is important. In vitro and in vivo data have shown that PTOs are nontoxic and nonmutagenic. However, these studies do not address interactions between PTOs and other compounds. The sulfur on PTOs may provide a novel reactive center on a DNA molecule for drug interactions. This study chose acetaminophen (ACAP) as a model drug because ACAP is oxidized to the reactive intermediate N-acetyl-p-benzoquinone imine (NAPQI), which reacts with sulfur-containing compounds.
Reaction of dCTP(S) with NAPQI or activated ACAP formed a product distinct from the reactants. Analysis of the product by fast atom bombardment mass spectroscopy gave a molecular weight consistent with NAPQI bound to a sulfur. Higher-molecular-weight products were seen on a polyacrylamide gel

electrophoresis after incubation of fluorescein-labeled PTO with NAPQI. These products were not seen after incubation of a phosphodiester **oligonucleotide** with NAPQI. 31P NMR analysis confirmed the existence of a heterogenous mixture of adducts between a PTO and NAPQI. Nonsequence-specific PTOs of various lengths were tested for their ability to reduce ACAP toxicity. Cell viability showed that larger PTOs provided greater protection. We evaluated the ability of NAPQI to cause mutations in the LacZ gene of pBluescript plasmid which contained phosphorothioate linkages at designed locations within the gene. In addition, the ability of ACAP to cause mutations in the HGPRT locus in cells grown in dATP(S)-containing medium was measured. No mutations were seen in either assay. Based upon these results, activated ACAP is reactive with PTOs in vitro, although this interaction is nontoxic and nonmutagenic.

L15 ANSWER 38 OF 74 MEDLINE
AN 95225822 MEDLINE
DN 95225822
TI [3'-(Tetrazol-2''-yl-3'-**deoxythymidine** and its 5''-substituted form: synthesis and conformation in the crystalline state. Substrate properties of 3'-(tetrazol-2''-yl)-3'-**deoxythymidine-5'-triphosphate** in relation to DNA polymerases].
3'-(Tetrazol-2''-il)-3'-dezoksitimidin i ego 5''-zameshchennye: sintez i konformatsiia v kristallicheskom sostoianii. Substratnye svoistva 3'-(tetrazol-2''-il)-3'-dezoksitimidin-5''-trifosfata po otnosheniiu k DNK-polimerazam.
AU Ostrovskii V A; Studentsov E P; Poplavskii V S; Ivanov N V; Gurskaia G V; Zavodnik V E; Ias'ko M V; Semizarov D G
SO BIOORGANICHESKAIA KHIMIIA, **(1995 Jan)** 21 (1) 49-54.
Journal code: 9Z8. ISSN: 0132-3423.
CY RUSSIA: Russian Federation
DT Journal; Article; (JOURNAL ARTICLE)
LA Russian
FS Priority Journals
EM 199507
AB 5''-Derivatives of 3'-(tetrazole-2''-yl)-3'-**deoxythymidines** were synthesized by interaction of 5'-benzoyl-2',3'-anhydrothymidine with tetrazole or its 5-derivatives followed by debenzoylation. Structures of two of them, 3'-(tetrazole-2''-yl)-3'-**deoxythymidine** and 3'-(5''-methyltetrazole-2''-yl)-3'-**deoxythymidine**, elucidated by X-ray analysis, revealed anti conformation of thymine about the glycosidic bond and 2'-endo-3'-exo-conformation of the sugar residue with gauche+ orientation with respect to C4'-C5'-bond. 3'-(Tetrazole-2''-yl)-3'-**deoxythymidine 5'-triphosphate** demonstrated poor substrate properties for the avian myeloblastosis virus reverse transcriptase and none for several other DNA polymerases.

L15 ANSWER 39 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1995:315534 CAPLUS
DN 122:133688
TI Preparation of boronated purine and pyrimidine bases, nucleosides, phosphate esters, and **oligomers** as drugs.
IN Spielvogel, Bernard F.; Sood, Anup; Hall, Iris H.; Shaw, Barbara Ramsay; Tomasz, Jeno
PA Boron Biologicals, Inc., USA; Duke University
SO PCT Int. Appl., 55 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 3

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9401413	A1	19940120	WO 1993-US6230	19930629 <--
	W: AU, CA, JP				

RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE
US 5362732 A 19941108 US 1992-909950 19920707 <--
AU 9346585 A1 19940131 AU 1993-46585 19930629 <--
EP 649411 A1 19950426 EP 1993-916875 19930629 <--
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE
PRAI US 1992-909950 19920707
US 1989-453311 19891220
WO 1993-US6230 19930629
OS CASREACT 122:133688; MARPAT 122:133688
AB Boronated purine and pyrimidine bases and boronated nucleosides, as well as phosphate esters and **oligomers** thereof, in which the boron-contg. substitutent is BH2CN, BH3, BF3, BH2CO2R, BH2CONHR (R = H, alkyl), were prepd. The compds. are boronated at a ring nitrogen of the purine or pyrimidine base, or at a 2', 3', or 5' amino substituent of the nucleoside sugar. Thus, 2'-**deoxyadenosine** and triphenylphosphine cyanoborane were stirred in DMF to give 11.3% N7-cyanoborano-2'-**deoxyadenosine** and 34.3% N1-cyanoborano-2'-**deoxyadenosine**. Adenine-N1-cyanoborane showed ED50 = 1.29 .mu.g/mL against murine L-1210. Title compds. also showed antiinflammatory, analgesic, and hypolipidemic activity. 2'-**Deoxyguanosine**-N7-cyanoborane-**5'-triphosphate** was used to prep. boronated **oligonucleotide** via PCR.

L15 ANSWER 40 OF 74 MEDLINE
AN 95001939 MEDLINE
DN 95001939
TI Interaction of the reverse transcriptase of human immunodeficiency virus type 1 with DNA.
AU Bakhanashvili M; Hizi A
CS Department of Cell Biology and Histology, Sackler School of Medicine, Tel Aviv University, Israel.
SO BIOCHEMISTRY, **(1994 Oct 11)** 33 (40) 12222-8.
Journal code: A0G. ISSN: 0006-2960.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199501
AB During DNA synthesis, the binding of human immunodeficiency virus (HIV) reverse transcriptase (RT) to the template-primer precedes its binding to **nucleotide** triphosphates. The interaction of **oligonucleotide** DNA with HIV-1 RT was investigated by using a gel retardation assay. Both homodimeric (p66/p66) and heterodimeric (p66/p51) isoforms of HIV-1 RT were capable of binding the DNA **oligomers**. Thus, all further studies on the interaction of HIV-1 RT with DNA were done with heterodimeric RT. We have studied the conditions for optimal binding. The formation of the RT-DNA complex was primer-independent, and the extent of DNA binding was indistinguishable for both single-stranded and double-stranded DNA (either blunt-ended or recessed). The DNA binding activity of the RT was found to be dependent on **oligonucleotide** length. HIV-1 RT binds DNA with no apparent sequence specificity. Hence, this enzyme belongs to the sequence nonspecific DNA binding proteins. The interaction was found to be independent of DNA synthesis. The formation of the RT-DNA complex was not influenced by the presence of either template-complementary or noncomplementary dNTPs, indicating that neither DNA polymerization nor binding of the RT to the dNTP affects the stability of the complex. The gel retardation assay was utilized to examine also the effect of various HIV-1 RT inhibitors (i.e., AZT-TP, ddTTP, TIBO, and 3,5,8-trihydroxy-4-quinolone) on the enzyme-DNA interaction. The results indicate differences in the modes of action of these compounds. (ABSTRACT TRUNCATED AT 250 WORDS)

L15 ANSWER 41 OF [redacted] MEDLINE
AN 94162216 MEDLINE
DN 94162216
TI Sensitivity of HIV-1 reverse transcriptase and its mutants to inhibition by azidothymidine triphosphate.
AU Carroll S S; Geib J; Olsen D B; Stahlhut M; Shafer J A; Kuo L C
CS Department of Biological Chemistry, Merck Research Labs, West Point, Pennsylvania 19486.
SO BIOCHEMISTRY, **(1994 Mar 1)** 33 (8) 2113-20.
Journal code: A0G. ISSN: 0006-2960.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199406
AB HIV-1 reverse transcriptase can catalyze the addition of either azidothymidine monophosphate (AZTMP) or thymidine monophosphate (dTMP) to a primer strand opposite template adenosine bases. The ratio of incorporation of AZTMP to dTMP as catalyzed by HIV-1 reverse transcriptase has been determined to be 0.4 using an RNA-DNA duplex substrate prepared from **oligonucleotides** with sequences taken from the HIV-1 genome sequence. Slight variations are found for the incorporation ratio of the two **nucleotides** on other substrates. Substrates containing more than one adenosine in the single-stranded part of the template allow for more chances to incorporate AZTMP and less full-length product. Variations in the intensity of bands on an autoradiograph of a DNA sequencing gel corresponding to different positions of incorporation of AZTMP suggest that not all template adenosine positions offer the same level of discrimination against incorporation of AZTMP. A reverse transcriptase containing a set of four mutations (D67N, K70R, T215Y, K219Q) known to cause resistance to AZT in cell culture assays has a ratio of incorporation that is 0.77 +/- 0.03 times the ratio for the wild-type reverse transcriptase opposite one specific template adenosine. In contrast, a hybrid mutant containing the same four mutations that cause resistance to AZT and an additional mutation, Y181C, which by itself causes resistance to the non-nucleoside inhibitor L-697,661 [Sardana et al. (1992), J. Biol. Chem. 267, 17526-17530], has a ratio of incorporation that is 1.34 +/- 0.01 times that of the wild-type, indicating that the hybrid mutant enzyme is more susceptible to inhibition by AZTTP than the wild-type reverse transcriptase.(ABSTRACT TRUNCATED AT 250 WORDS)

L15 ANSWER 42 OF 74 MEDLINE
AN 94124510 MEDLINE
DN 94124510
TI Mispair-, site-, and strand-specific error rates during simian virus 40 origin-dependent replication in vitro with excess **deoxythymidine** triphosphate.
AU Roberts J D; Izuta S; Thomas D C; Kunkel T A
CS Laboratory of Molecular Genetics, National Institute of Environmental Health Sciences, Research Triangle Park, North Carolina 27709.
SO JOURNAL OF BIOLOGICAL CHEMISTRY, **(1994 Jan 21)** 269 (3) 1711-7.
Journal code: HIV. ISSN: 0021-9258.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 199405
AB We have measured the fidelity of leading and lagging strand DNA replication in HeLa cell extracts. Providing an excess of one dNTP in reactions induces replication errors consistent with misincorporation of that dNTP. With excess dTTP, both substitutions and single-

nucleotide frameshifts are induced. Error distribution is nonrandom; reproducible hot spots for a substitution and a frameshift error are observed. Measurements with two vectors having the origin of replication on opposite sides of the mutational target demonstrate that error rates for G.dTTP and C.dTTP mispairs depend on whether the strand is replicated as the leading or lagging strand. Also, the two hot spots are only observed in one origin-target orientation. Replication reactions reconstituted from two fractions derived from extracts are 3-fold less accurate, but the error specificity with excess dTTP is similar to that with extracts. This suggests that the processes responsible for the nonrandom error rates are not lost as a result of fractionation. Furthermore, the reconstituted system is devoid of mismatch repair activity. Thus, mismatch repair is not responsible for the mispair-, site-, and strand-specific differences observed.

L15 ANSWER 43 OF 74 MEDLINE
AN 94306633 MEDLINE
DN 94306633
TI Synthesis of a 25 base **oligonucleotide** containing a styrene oxide modification at the O6 position of 2'-**deoxyguanosine** at a defined site and incorporation studies of the similarly modified 2'-**deoxyguanosine-5'-triphosphate**.
AU Pongracz K; Dosanjh M K; Singer B; Bodell W J
CS Department of Neurological Surgery, University of California San Francisco, School of Medicine 94143-0806.
NC P24ES04705 (NIEHS)
CA 42736 (NCI)
RR01614 (NCRR)
SO CARCINOGENESIS, **(1994 Jul)** 15 (7) 1371-5.
Journal code: C9T. ISSN: 0143-3334.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 199410
AB A diastereomeric mixture of the regioisomers O6-(2-hydroxy-2-phenylethyl)-2'-**deoxyguanosine** (st6G, beta-isomer) and O6-(2-hydroxy-1-phenylethyl)-2'-**deoxyguanosine** (alpha-isomer) was site-specifically placed in a 25 base **oligonucleotide** template 5'-CCGCTAst6GCGGGTACCGAGCTCGAAT-3' using CED phosphoramidite chemistry. Using 32P-post-labeling we found the **oligonucleotide** to contain 95% of the beta-isomer and 5% of the alpha-isomer of st6G. st6G as the 3'-phosphate was found to be considerably more acid labile than O6-methyl-2'-**deoxyguanosine**-3'-phosphate, leading to dealkylation during **oligonucleotide** synthesis. The diastereomeric mixture of O6-(2-hydroxy-2-phenylethyl)-2'-deoxy-guanosine-**5'-triphosphate** (st6dGTP) was chemically synthesized and used as a substrate for the exonuclease-free Klenow fragment of Escherichia coli DNA polymerase I. This study demonstrated that st6dGTP could be incorporated opposite **deoxycytidine** and did not completely block replication.

L15 ANSWER 44 OF 74 MEDLINE
AN 94234989 MEDLINE
DN 94234989
TI Chiral discrimination of enantiomeric 2'-**deoxythymidine** **5'-triphosphate** by HIV-1 reverse transcriptase and eukaryotic DNA polymerases.
AU Yamaguchi T; Iwanami N; Shudo K; Saneyoshi M
CS Department of Biological Sciences, Nishi-Tokyo University, Yamanashi, Japan.
SO BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, **(1994 Apr 29)**

200 (2) 1023
Journal code: [illegible]9Y8. ISSN: 0006-291X.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 199408
AB Inhibitory effects of 2'-deoxy-L-thymidine 5'-**triphosphate** (L-dTTP), the enantiomer of the natural substrate D-dTTP, on the activity of mammalian DNA polymerases alpha, beta and gamma, Escherichia coli DNA polymerase I and human immunodeficiency virus 1 (HIV-1) reverse transcriptase were examined. When poly(rA)n-**oligo**(dT)12-18 was used as the template-primer, L-dTTP showed remarkable inhibitory effect on HIV-1 reverse transcriptase in competitive fashion with respect to the substrate dTTP. In contrast, L-dTTP did not inhibit DNA polymerases alpha and was slightly inhibitory to DNA polymerase beta. These results suggest that the nuclear DNA polymerases alpha and beta showed high specificity for the substrate with the natural configuration of the sugar moiety, D-dTTP, exhibiting little or no ability to recognize L-dTTP, whereas HIV-1 reverse transcriptase essentially lacked the ability to differentiate the D- and L-sugar moieties.

L15 ANSWER 45 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1994:548543 CAPLUS
DN 121:148543
TI 2-Chloro-2'-**deoxyadenosine** monophosphate residues in DNA enhance susceptibility to 3' .fwdarw. 5' exonucleases
AU Hentosh, Patricia; Grippo, Paul
CS Dep. Pharmacology Molecular Biol., Chicago Med. Sch., North Chicao, IL, 60064, USA
SO Biochem. J. (**1994**), 302(2), 567-71
CODEN: BIJOAK; ISSN: 0264-6021
DT Journal
LA English
AB 2-Chloro-2'-**deoxyadenosine** triphosphate, a purine **nucleotide** analog and potent antileukemic agent, was incorporated into double-stranded 36-mers in place of dATP to investigate the effects of 2-chloroadenine (ClAde) on DNA polymerase-assocd. 3' .fwdarw. 5' exonuclease activity. ClAde residues within one strand of duplex DNA did not inhibit exonuclease activity; on the contrary, ClAde-contg. minus strands were digested to a greater extent than was control DNA in the absence of deoxyribonucleoside triphosphates by Escherichia coli Klenow fragment, yeast DNA polymerase II and T4 DNA polymerase. After a 30 min incubation with 5 units of Klenow fragment, .apprx.65% of control DNA remained in DNA fragments of 26 bases or larger compared with only .apprx.25% of ClAde-substituted substrate. Unsubstituted plus strands opposite a ClAde-contg. strand were likewise digested more quickly by 3' .fwdarw. 5' exonuclease, but only in the vicinity of the ClAde sites. Approx. 63% of the plus strands from ClAde-contg. **oligomers** were less than 24 bases in length after a 25 min digestion period with Klenow fragment compared with only .apprx.32% of control DNA. Such results indicate that, unlike other base modifications such as pyrimidine dimers, methoxy psoralen adducts and certain nucleoside analogs, all of which inhibit or decrease the rate of strand degrdn. by 3' .fwdarw. 5' exonucleases, incorporated ClAde enhances strand degrdn. of duplex DNA.

L15 ANSWER 46 OF 74 MEDLINE
AN 94340558 MEDLINE
DN 94340558
TI Miscoding during DNA synthesis on damaged DNA templates catalysed by mammalian cell extracts.
AU Shibutani S; Grollman A P
CS Department of Pharmacological Sciences, State University of New York at

Stony Brook [illegible]4-8651.
SO CANCER LETTERS, **(1994 Aug 15)** 83 (1-2) 315-22.
Journal code: CMX. ISSN: 0304-3835.
CY Ireland
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 199411
AB **Oligodeoxynucleotides**, modified site-specifically with 7,8-dihydro-8-oxodeoxyguanosine (8-oxodG), 7,8-dihydro-8-oxoadenosine (8-oxodA) and 6-O-methyldeoxyguanosine (O6medG), were used as templates for DNA synthesis in primer-extension reactions catalysed by extracts prepared from human (HeLa) cells, simian kidney (COS-7) cells and various mouse tissues. Fully-extended reaction products were analysed by two-phase polyacrylamide gel electrophoresis (Shibutani, Chem. Res. Toxicol. 6, 625, 1993). Using extracts prepared from HeLa or COS-7 cells, dAMP was preferentially incorporated opposite 8-oxodG; dTMP was incorporated opposite 8-oxodA and dTMP, accompanied by small amounts of dCMP, was incorporated opposite O6medG. Translesional synthesis was strongly inhibited by N-ethylmaleimide and partially inhibited by N-butylphenyl-dGTP. This model system can be used to predict the mutagenic potential of selectively-damaged DNA in mammalian cells.

L15 ANSWER 47 OF 74 MEDLINE
AN 93208125 MEDLINE
DN 93208125
TI Replication of the base pair 6-thioguanine/5-methyl-2-pyrimidine with the large Klenow fragment of Escherichia coli DNA polymerase I.
AU Rappaport H P
CS Biology Department, Temple University, Philadelphia, Pennsylvania 19122.
SO BIOCHEMISTRY, **(1993 Mar 30)** 32 (12) 3047-57.
Journal code: A0G. ISSN: 0006-2960.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199307
AB The kinetics and the fidelity of replication of the base pair 6-thioguanine (Gs)/5-methyl-2-pyrimidinone (Th) have been determined by using defined **oligomers** with the large Klenow fragment of Escherichia coli DNA polymerase I. The insertion efficiency, Vmax/Km (min-1 microM-1), of Th opposite Gs is 1.5 and the insertion efficiency of Gs opposite Th is 0.7. By comparison, the insertion efficiencies of C opposite G and G opposite C are 0.5 and 1.5. The insertion efficiency of the next base, A opposite T, is 2 times greater after the base pair Gs/Th than after G/C. The fidelity of replication with respect to thymine and adenine has misinsertion frequencies, or ratios of the insertion efficiency of the "wrong" base to the "right" base, of 7 x 10(-4) for T opposite Gs (T/Gs), 4 x 10(-6) for T/Th, and a maximum stable misinsertion frequency of 4 x 10(-4) for A/Th. No detectable elongation occurs after an A is inserted opposite a Gs. These values are similar to the misinsertion frequencies of G and C with T and A. The maximum stable misinsertion frequencies with G and C are 4 x 10(-2) for G/Th, 3 x 10(-2) -7 x 10(-3) for Gs/C, and 2.6 x 10(-1) for C/Gs, and the misinsertion frequency is < 1 x 10(-3) for Th/G. The kinetics results and molecular modeling suggest modifications to the Gs/Th base pair that may provide higher levels of fidelity of replication with respect to C and G.

L15 ANSWER 48 OF [redacted] MEDLINE
AN 94027935 MEDLINE
DN 94027935
TI Use of random primer extension for concurrent amplification and nonradioactive labeling of nucleic acids.
AU Mackey J; Darfler M; Nisson P; Rashtchian A
CS Research Products Division, Life Technologies, Inc., Gaithersburg, Maryland 20884-9880..
SO ANALYTICAL BIOCHEMISTRY, **(1993 Aug 1)** 212 (2) 428-35.
Journal code: 4NK. ISSN: 0003-2697.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199401
AB A method for efficient nonradioactive labeling of DNA with biotin using random primer extension has been developed. Under the conditions described, a significant amount of DNA synthesis occurs during incorporation of the nonradioactive label, resulting in amplification of the original template DNA. The effect of primer size, substrate concentration, enzyme concentration, and ratio of biotinylated **nucleotide** to normal **nucleotide** on the amount of DNA synthesis was determined. Amplifications of 10- to > 300-fold were attained, depending on the starting template concentration. Template may be varied from 1 to 500 ng per reaction. The size of the resulting biotinylated probes is 100-1000 **nucleotides** with a significant proportion in the 100-300 **nucleotide** range. The biotinylated probes were used to detect single-copy genes on Southern blot hybridizations and to identify specific loci in metaphase chromosome spreads by in situ hybridization followed by fluorescent detection with streptavidin-fluorescein isothiocyanate. Random primer amplification and labeling provides a convenient method for preparation of biotinylated probes from small amounts of template DNA.

L15 ANSWER 49 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1993:449812 CAPLUS
DN 119:49812
TI Specific synthesis of adenosine(5')tetraphospho(5')nucleoside and adenosine(5')**oligophospho**(5')adenosine (n > 4) catalyzed by firefly luciferase
AU Ortiz, Begona; Sillero, Antonio; Gunther Sillero, Maria A.
CS Fac. Med., Univ. Auton. Madrid, Madrid, E-28029, Spain
SO Eur. J. Biochem. **(1993)**, 212(1), 263-70
CODEN: EJBCAI; ISSN: 0014-2956
DT Journal
LA English
OS CASREACT 119:49812
AB Luciferase catalyzes the preferential synthesis of adenosine(5')tetraphospho(5')nucleoside (Ap4N) in the presence of luciferin (LH2), adenosine 5'-[.gamma.-thio]triphosphate (ATP[.gamma.S] and NTP (other than ATP), with very low, or undetectable synthesis of Ap4A or Np4N, because ATP[.gamma.S] is a good adenylyl donor for the formation of the E-LH2-AMP complex, but a poor adenylyl acceptor from the complex, and NTP, other than ATP, are bad **nucleotidyl** donors, but good acceptors of the AMP moiety of the E-LH2-AMP complex. Synthesis of the corresponding Ap4N (or Ap5G in the case of p4G were obtained in the presence of ATP[.gamma.S] and GTP, UTP, CTP, XTP, dTTP, ITP, dGTP, dCTP, dITP, .epsilon.ATP (.epsilon.A, N6-ethenoadenosine) or p4G. The yield of synthesis of AP4N was at least 50% of that theor. expected. The process can be easily scaled-up, which allows synthesis of at least 1-5 .mu.mol Ap4N. Further evidence for the synthesis of Ap4G from ATP[.gamma.S] and GTP was obtained by 1H-NMR and 31P-NMR spectroscopy. Synthesis of Ap4N, in yields lower than those above, can also be obtained in the presence of ADP and NTP; synthesis is due to the presence in com. luciferase of enzyme

(adenylate ki[redacted]e and NDP kinase) that catalyz[redacted]he synthesis of ATP from ADP and NTP. In the presence of ATP and polyp[redacted]sphate, luciferase catalyzes the synthesis of a variety of compds. of adenosine 5'-polyphosphates (pnA; n=3-20 and ApnA; n=4-16). In the presence of P3 of P4, preferential synthesis of p4A and Ap5A or p5A and Ap6A were obtained, resp., showing that both polyphosphates accept the adenylyl moiety of the E-LH2-AMP complex. Polyphosphates of chain length 5, 15 and 35 elicited the synthesis of a variety of PnA and ApnA. Ap4A is also split by luciferase in the presence of P3 or P4 (but not in the presence of P5) yielding preferential synthesis of p4A and Ap5A, or p5A and Ap6A, resp.

L15 ANSWER 50 OF 74 MEDLINE
AN 93307502 MEDLINE
DN 93307502
TI Interactions of the HIV-1 reverse transcriptase 'AZT-resistant' mutant with substrates and AZT-TP.
AU Pokholok D K; Gudima S O; Yesipov D S; Dobrynin V N; Rechinsky V O; Kochetkov S N
CS V.A. Engelhardt Institute of Molecular Biology, Russian Academy of Sciences, Moscow.
SO FEBS LETTERS, **(1993 Jul 5)** 325 (3) 237-41.
Journal code: EUH. ISSN: 0014-5793.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 199310
AB To investigate the biochemical basis of the HIV-1 resistance to AZT we obtained the RT mutant containing four amino acid substitutions by an **oligonucleotide**-directed mutagenesis technique. Enzymatic properties of the wild type and mutant RTs were compared. 'AZT-resistant' mutations in RT were shown to be associated with the reduced capability of AZT-TP to block the DNA- but not RNA-directed DNA synthesis.

L15 ANSWER 51 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1994:97363 CAPLUS
DN 120:97363
TI Sequence-specific DNA damage using iodine-125-labeled antisense **oligonucleotides**
AU England, Phillip R.; Murray, Vincent
CS Sch. Biochem. Mol. Genet., Univ. New South Wales, Kensington, 2033, Australia
SO Antisense Res. Dev. (**1993**), 3(2), 219-24
CODEN: AREDEI; ISSN: 1050-5261
DT Journal
LA English
AB A procedure is described that cleaves single-stranded DNA with sequence specificity. This process involves attaching a DNA damaging agent to an **oligonucleotide**. This **oligonucleotide** delivers the DNA damaging agent, iodine-125, to a specific DNA sequence by complementary hybridization. 5-[125I]Iodo-2-**deoxycytidine 5'-triphosphate** was enzymically incorporated into an **oligonucleotide** that was designed to hybridize to a single-stranded DNA target. 125I decays by electron capture and causes breaks in the target DNA. These breaks were obsd. on a DNA sequencing gel. After 22 days of exposure to the 125I-labeled **oligonucleotide**, significant damage was obsd. within 1 to 2 bases of the expected site of hybridization. Densitometry showed that after 48 days the amt. of damage had approx. doubled. This method facilitates easy design and testing of **oligonucleotides** that could potentially be used to inactivate gene expression in a wide variety of organisms.

L15 ANSWER 52 OF 74 MEDLINE
AN 93326106 MEDLINE
DN 93326106
TI Bcl-2 oncogene protects a bone marrow-derived pre-B-cell line from 5'-fluor,2'-deoxyuridine-induced apoptosis.
AU Oliver F J; Marvel J; Collins M K; Lopez-Rivas A
CS Instituto de Parasitologia Lopez Neyra, Consejo Superior de Investigaciones Cientificas (CSIC), Granada, Spain.
SO BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, **(1993 Jul 15)** 194 (1) 126-32.
Journal code: 9Y8. ISSN: 0006-291X.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 199310
AB The bcl-2 protooncogene has been shown to protect haemopoietic precursors from programmed cell death after the removal of interleukin-3 (IL3). In the present report we show evidence that overexpression of bcl-2 in the pre-B-cell line BAF3 protects cells from apoptosis induced by treatment with the thymydilate synthase inhibitor 5'-fluor,2'-deoxyuridine (FDUR) in the presence of IL-3. Dose-response experiments analyzing the dependence of cell death on drug concentration indicated a marked resistance of BAF3bcl-2 to FDUR treatment. Cleavage of DNA into **oligonucleosome** -length fragments, a characteristic of apoptosis, was observed in BAF3 cells and inhibited in the cells overexpressing bcl-2. We have determined variations in the dATP and dTTP pools after FDUR treatment. Interestingly, no differences were found between both cells in the kinetics of changes in dNTP pools. Therefore, the protective effect of the Bcl-2 protein on apoptosis induced by dNTP unbalance must be ascribed to a step downstream of perturbations in the synthesis of DNA precursors and before activation of endonucleolytic cleavage of chromatin.

L15 ANSWER 53 OF 74 CAPLUS COPYRIGHT 2000 ACS DUPLICATE 7
AN 1993:466307 CAPLUS
DN 119:66307
TI Activity of human DNA polymerases .alpha. and .beta. with 2-chloro-2'-**deoxyadenosine 5'-triphosphate** as a substrate and quantitative effects of incorporation on chain extension
AU Chunduru, Srinivas K.; Appleman, James R.; Blakley, Raymond L.
CS Dep. Biochem. Clin. Pharmacol., St. Jude Child. Res. Hosp., Memphis, TN, 38101, USA
SO Arch. Biochem. Biophys. (**1993**), 302(1), 19-30
CODEN: ABBIA4; ISSN: 0003-9861
DT Journal
LA English
AB When 2-chloro-2'-**deoxyadenosine 5'-triphosphate** (CldATP) is incorporated into DNA by human polymerases .alpha. and .beta. (Hpol.alpha., Hpol.beta.) the rate of chain extension decreases. In the present study primer extension has been quantitated by estg. the concn. of each successive **oligonucleotide** product at a series of time points. This has permitted calcn. of pseudo-first-order rate consts. for successive **nucleotide** addns. to primer. By this method it has been shown that rate consts. for CldATP addn. are 79-100% of those for dATP in the case of Hpol.alpha., and 26-153% with Hpol.beta.. The concns. of CldATP for half max. velocity is 0.6 .mu.M for Hpol.alpha., and 6 .mu.M for Hpol.beta., each about twice the value for dATP. Thus, CldATP is a good substrate for both enzymes but is more efficiently used by Hpol.alpha.. Addn. of a single analog residue

by Hpol.beta any of seven primers decrease the rate const. for addn. of the next **nucleotide** to 2-7% of that after dTTP addn. and further extension is negligible. Consecutive addns. of analog residues by Hpol.alpha. progressively decrease the rate of subsequent extension, and after five consecutive addns. extension virtually terminates. These effects probably make a major contribution to the cytotoxicity of chlorodeoxyadenosine and its therapeutic usefulness as an antileukemic agent.

L15 ANSWER 54 OF 74 MEDLINE
AN 93094202 MEDLINE
DN 93094202
TI Beta-L-thymidine **5'-triphosphate** analogs as DNA polymerase substrates.
AU Van Draanen N A; Tucker S C; Boyd F L; Trotter B W; Reardon J E
CS Division of Experimental Therapy, Wellcome Research Laboratories, Research Triangle Park, North Carolina 27709.
SO JOURNAL OF BIOLOGICAL CHEMISTRY, **(1992 Dec 15)** 267 (35) 25019-24.
Journal code: HIV. ISSN: 0021-9258.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 199303
AB beta-L-3'-**Deoxythymidine 5'-triphosphate** (L-ddTTP) and beta-L-3'-deoxy-2',3'-didehydrothymidine **5'-triphosphate** (L-d4TTP) were substrates for human immunodeficiency virus reverse transcriptase, Escherichia coli DNA polymerase I (Klenow), and Sequenase (modified T7 DNA polymerase). The beta-D- and beta-L-enantiomers of 5-methyluridine **5'-triphosphate** (rTTP) were inhibitors but not substrates of reverse transcriptase. The steady-state Km values for L-ddTTP and L-d4TTP, with all three enzymes, were 12-70-fold larger than the Km values for the corresponding D-enantiomers. The Km value of reverse transcriptase for L-ddTTP was 50-fold larger than that for D-ddTTP because the Kd for L-ddTTP was 5-fold larger than that for D-ddTTP, and the first-order rate constant for incorporation of L-ddTMP into the template-primer was 10% that of the D-enantiomer. The D- and L-enantiomers had kcat values with reverse transcriptase and Sequenase that were similar to kcat for the natural substrate, thymidine **5'-triphosphate** (dTTP). Thus, the rate determining step appeared to be dissociation of the enzyme-chain-terminated template-primer complex. In contrast, kcat values for the L-enantiomers with Klenow were only 0.1% that of dTTP, and the kcat values for the D-enantiomers were 15% the kcat for dTTP. The reduced kcat values were due to a change in rate determining step from dissociation of the Klenow-chain-terminated template-primer complex to an earlier step in the reaction mechanism, presumably catalysis. Thus, these DNA polymerases did not stereospecifically recognize D-nucleoside **5'-triphosphate** analogs as substrates...

L15 ANSWER 55 OF 74 MEDLINE
AN 93003068 MEDLINE
DN 93003068
TI Minimal kinetic mechanism for misincorporation by DNA polymerase I (Klenow fragment).
AU Eger B T; Benkovic S J
CS Davey Laboratory, Department of Chemistry, Pennsylvania State University, University Park 16802.
NC GM13306 (NIGMS)
SO BIOCHEMISTRY, **(1992 Sep 29)** 31 (38) 9227-36.

Journal code: A0G. ISSN: 0006-2960.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199301
AB The minimal kinetic mechanism for misincorporation of a single **nucleotide** (dATP) into a short DNA primer/template (9/20-mer) by the Klenow fragment of DNA polymerase I [KF(exo+)] has been previously published [Kuchta, R. D., Benkovic, P., & Benkovic, S.J. (1988) Biochemistry 27, 6716-6725]. In this paper are presented refinements to this mechanism. Pre-steady-state measurements of correct **nucleotide** incorporation (dTTP) in the presence of a single incorrect **nucleotide** (dATP) with excess KF-(exo+) demonstrated that dATP binds to the KF(exo+)-9/20-mer complex in two steps preceding chemistry. Substitution of (alpha S)dATP for dATP yielded identical two-step binding kinetics, removing **nucleotide** binding as a cause of the elemental effect on the rate of misincorporation. Pyrophosphate release from the ternary species [KF'(exo+)-9A/20-mer-PPi] was found to occur following a rate-limiting conformational change, with this species partitioning equally to either **nucleotide** via internal pyrophosphorolysis or to misincorporated product. The rate of 9A/20-mer dissociation from the central ternary complex (KF'-9A/20-mer-PPi) was shown to be negligible relative to exonucleolytic editing. Pyrophosphorolysis of the misincorporated DNA product (9A/20-mer), in conjunction with measurement of the rate of dATP misincorporation, permitted determination of the overall equilibrium constant for dATP misincorporation and provided a value similar to that measured for correct incorporation. A step by step comparison of the polymerization catalyzed by the Klenow fragment for correct and incorrect **nucleotide** incorporation emphasizes that the major source of the enzyme's replicative fidelity arises from discrimination in the actual chemical step and from increased exonuclease activity on the ternary misincorporated product complex owing to its slower passage through the turnover sequence.

L15 ANSWER 56 OF 74 MEDLINE
AN 92256376 MEDLINE
DN 92256376
TI Human immunodeficiency virus reverse transcriptase: steady-state and pre-steady-state kinetics of **nucleotide** incorporation.
AU Reardon J E
CS Division of Experimental Therapy, Wellcome Research Laboratories, Research
Triangle Park, North Carolina 27709.
SO BIOCHEMISTRY, **(1992 May 12)** 31 (18) 4473-9.
Journal code: A0G. ISSN: 0006-2960..
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199208
AB Steady-state and pre-steady-state kinetic constants were determined for reverse transcriptase catalyzed incorporation of **nucleotides** and **nucleotide** analogues into defined-sequence DNA primed-RNA templates. 3'-Azido-3'-**deoxythymidine 5'-triphosphate** (AZTTP) was almost as efficient a substrate (kcat/Km) as dTTP for the enzyme. In contrast, the four 2',3'-dideoxynucleoside **5'-triphosphates** and 3'-deoxy-2',3'-didehydrothymidine **5'-triphosphate** (d4TTP) were 6-30-fold less efficient substrates of the enzyme. The kcat values for all **nucleotide** analogues were similar, consistent with a kinetic model in which the steady-state rate-limiting step was dissociation of the template-primer from the enzyme [Reardon, J. E., & Miller, W. H. (1990) J. Biol. Chem. 265, 20302-20307]. The pre-steady-state kinetics of single-

nucleotide incorporation were consistent with a kinetic model: [formula: see text] where E, TP, and dNTP represent reverse transcriptase, a defined-sequence DNA primed-RNA template, and 2'-deoxynucleoside **5'-triphosphate** (or analogue), respectively. The dissociation constant (Kd1) for template-primer binding was 10 nM, and the estimated rate constants for association and dissociation of the enzyme.template-primer complex were 4 x 10(6) M-1 s-1 and 0.04 s-1, respectively. The dissociation constants (Kd2) for dTTP, AZTTP, and 3'-**deoxythymidine 5'-triphosphate** (ddTTP) were 9, 11, and 4.6 microM, respectively. Thus, the differences in steady-state Km values were not due to differences in binding of the **nucleotide** analogues to the enzyme. In contrast, the rate-limiting step during single-**nucleotide** incorporation (kp) was sensitive to the structure of the **nucleotide** substrate. (ABSTRACT TRUNCATED AT 250 WORDS)

L15 ANSWER 57 OF 74 CAPLUS COPYRIGHT 2000 ACS DUPLICATE 8
AN 1992:645058 CAPLUS
DN 117:245058
TI Inhibition of reverse transcriptase from feline immunodeficiency virus by analogs of 2'-**deoxyadenosine 5'-triphosphate**
AU Cronn, Richard C.; Remington, Kathryn Martin; Preston, Bradley D.; North, Thomas W.
CS Div. Biol. Sci., Univ. Montana, Missoula, MT, 59812, USA
SO Biochem. Pharmacol. (**1992**), 44(7), 1375-81
CODEN: BCPCA6; ISSN: 0006-2952
DT Journal
LA English
AB The replication of feline immunodeficiency virus (FIV) in cultured cells was inhibited by 2',3'-dideoxyadenosine (ddA) and by 9-(2-phosphonylmethoxyethyl)adenine (PMEA), with IC50 values of 0.98 and 0.95 .mu.M, resp. The effects of the presumed active forms of these inhibitors, ddATP and PMEA diphosphate (PMEApp), upon the FIV reverse transcriptase (RT) were examd. with 2 different template-primer systems. Both of these compds. were potent inhibitors of the FIV RT in reactions with primed .vphi.X-174 DNA, yielding Ki values of 8.8 nM for ddATP and 5.0 nM for PMEApp. However, they were both poor inhibitors of the reaction with poly(rU)-**oligo**(dA); concns. of ddATP or PMEApp >10 .mu.M were required to inhibit this reaction by 50%. Further anal. of the reaction with poly(rU)-**oligo**(dA) revealed that even in the absence of inhibitors the primers were extended by <20 **nucleotides**. In contrast, high-mol.-wt. products were obtained in reactions with .vphi.X-174 DNA. These results suggest that the reaction of FIV RT with poly(rU)-**oligo**(dA) is not highly processive. The high degree of termination encountered during this reaction with poly(rU)-**oligo**(dA) may be responsible for the low inhibitory potential of ddATP and PMEApp.

L15 ANSWER 58 OF 74 CAPLUS COPYRIGHT 2000 ACS DUPLICATE 9
AN 1992:75741 CAPLUS
DN 116:75741
TI The observed inhibitory potency of 3'-azido-3'-**deoxythymidine 5'-triphosphate** for HIV-1 reverse transcriptase depends on the length of the poly(rA) region of the template
AU Ma, Qi Feng; Bathurst, Ian C.; Barr, Philip J.; Kenyon, George L.
CS Dep. Pharm. Chem., Univ. California, San Francisco, CA, 94143, USA
SO Biochemistry (**1992**), 31(5), 1375-9
CODEN: BICHAW; ISSN: 0006-2960
DT Journal
LA English
AB The inhibitory potency of 3'-azido-3'-**deoxythymidine 5**

'-triphospha (AZTTP) against HIV-1 reverse nscriptase (HIV-1 RT) was further evaluated. The results indicate that the previously reported low Ki values for AZTTP against HIV-1 RT (2-35 nM) are due neither to the direct tight binding of AZTTP to HIV-1 RT nor to the interaction of the enzyme with AZTMP moiety terminated primer-templates, but instead they are an artifact of the use of a homotemplate-primer [poly(rA).cntdot.**oligo**(dT)]. With a set of RNAs of defined sequence as templates, it was demonstrate that the obsd. Ki value for AZTTP depends on the length of the poly(rA) region following the primer in the RNA template. The more adenosyl residue in the RNA template that are available for processing incorporation of TMP moieties, the lower is the obsd. Ki value for AZTTP. Since the potencies of new inhibitors of HIV-1 RT are usually compared with that for AZTTP, these results have important consequences for the process of discovery of new HIV inhibitors that are of potential use in AIDS therapy.

L15 ANSWER 59 OF 74 MEDLINE
AN 92112818 MEDLINE
DN 92112818
TI Interactions of azidothymidine triphosphate with the cellular DNA polymerases alpha, delta, and epsilon and with DNA primase.
AU Nickel W; Austermann S; Bialek G; Grosse F
CS Max-Planck-Institut fur Experimentelle Medizin, Abetilung Chemie, Gottingen, Germany.
SO JOURNAL OF BIOLOGICAL CHEMISTRY, **(1992 Jan 15)** 267 (2) 848-54.
Journal code: HIV. ISSN: 0021-9258.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 199204
AB The interactions of azidothymidine triphosphate, the metabolically active form of the anti-AIDS drug azidothymidine (zidovudine), with the cellular DNA polymerases alpha, delta, and epsilon, as well as with the RNA primer-forming enzyme DNA primase were studied in vitro. DNA polymerase alpha was shown to incorporate azidothymidine monophosphate into a growing polynucleotide chain. This occurred 2000-fold slower than the incorporation of natural dTTP. Despite the ability of polymerase alpha to use azidothymidine triphosphate as an alternate substrate, this compound was only marginally inhibitory to the enzyme (Ki greater than 1 mM). Furthermore, the DNA primase activity associated with DNA polymerase alpha was barely inhibited by azidothymidine triphosphate (Ki greater than 1 mM). Inhibition was more pronounced for DNA polymerases delta and epsilon.
The type of inhibition was competitive with respect to dTTP, with Ki values of 250 and 320 microM, respectively. No incorporation of azidothymidine monophosphate was detectable with these two DNA polymerases because their associated 3'- to 5'-exonuclease activities degraded primer molecules prior to any measurable elongation. Template-primer systems with a preformed 3'-azidothymidine-containing primer terminus inhibited the three replicative polymerases rather potently. DNA polymerase alpha was inhibited with a Ki of 150 nM and polymerases delta and epsilon with Ki values of 25 and 20 nM, respectively. The type of inhibition was competitive with respect to the unmodified substrate poly(dA).**oligo**(dT) for all DNA polymerases tested. Performed 3'-azidothymidine-containing primers hybridized to poly(dA) were rather resistant to degradation by the 3'- to 5'-exonuclease of DNA polymerases epsilon and more susceptible to the analogous activity that copurified with DNA polymerase delta. It is proposed that the repair of

3'-azidothymidine-containing primers might become rate-limiting for the process of DNA replication in cells that have been treated with azidothymidine triphosphate.

L15 ANSWER 60 OF 74 MEDLINE
AN 92252618 MEDLINE
DN 92252618
TI Expression of IGF-1 mRNA in the murine subventricular zone during postnatal development.
AU Bartlett W P; Li X S; Williams M
CS Department of Neuroscience and Anatomy, Hershey Medical Center, Pennsylvania State University, Hershey 17033.
SO BRAIN RESEARCH. MOLECULAR BRAIN RESEARCH, **(1992 Feb)** 12 (4) 285-91.
Journal code: MBR. ISSN: 0169-328X.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199208
AB Insulin-like growth factor-1 (IGF-1) stimulates the proliferation and maturation of neuroglia in vitro. To further investigate its role in gliogenesis, in situ hybridization was utilized to determine whether IGF-1 mRNA was expressed in the subventricular zone (SVZ) of the postnatal mouse forebrain. The SVZ is a transient germinal zone and in the neonate is the principle source of **oligodendroglia** for myelinating fiber tracts of the forebrain. Strong hybridization signal was detected over cells in the SVZ at postnatal day (PND) 4, the earliest time point examined. Positive signal persisted in the SVZ at PND 8, however, the number of IGF-1-labeled cells declined rapidly during the second postnatal week. IGF-1 mRNA was not uniformly distributed throughout the SVZ and the majority of labeled cells were located within its so-called 'border' region. In contrast to the SVZ, IGF-1 mRNA-expressing cells were only rarely found in forebrain fiber tracts. IGF-1 transcripts were not detected in ependymal lining or choroid plexus of the lateral ventricle. In light of its known gliotrophic activity, the localization of IGF-1 mRNA in the SVZ suggests that locally produced IGF-1 may act as a mitogen or differentiation-inducing agent during gliogenesis.

L15 ANSWER 61 OF 74 MEDLINE
AN 93037380 MEDLINE
DN 93037380
TI A new and potent 2-5A analogue which does not require a 5'-polyphosphate to activate mouse L-cell RNase L.
AU Torrence P F; Brozda D; Alster D K; Pabuccuoglu A; Lesiak K
CS Section on Biomedical Chemistry, National Institute of Diabetes and Digestive and Kidney Diseases, National Institutes of Health, Bethesda, MD 20892..
SO ANTIVIRAL RESEARCH, **(1992 Jun)** 18 (3-4) 275-89.
Journal code: 6I7. ISSN: 0166-3542.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199301
AB In order to explore the possibility of supplanting the requirement of a **5'-triphosphate** moiety for the activation of the 2-5A-dependent endonuclease (RNase L) of mouse L-cells, two new tetrameric analogues of 2-5A were synthesized. The first tetramer, obtained by both a

modified prebiotic synthetic approach as well as a phosphite triester solid phase **oligonucleotide** synthesis method, [redacted]s p5'A2'p5'A2'p5'(br8A)2'p5'(br8A). The second **oligonucleotide** was derived from the former by a sequence involving periodate oxidation, reaction with n-hexylamine, and cyanoborohydride reduction, resulting in conversion of the 2'-terminal adenosine residue to 9-(3'-aza-4'-hexyl-1',2',3',4'-tetradeoxyhexopyranos-1(1')-yl)-8-++ +bromoadenine. Both of these **oligomers**, bearing only 5'-monophosphate groups, were found to be as potent as 2-5A itself as activators of the RNase L of mouse L-cells.

L15 ANSWER 62 OF 74 MEDLINE
AN 93072902 MEDLINE
DN 93072902
TI Quantification of gene expression over a wide range by the polymerase chain reaction.
AU Kinoshita T; Imamura J; Nagai H; Shimotohno K
CS Virology Division, National Cancer Center Research Institute, Tokyo, Japan.
SO ANALYTICAL BIOCHEMISTRY, **(1992 Nov 1)** 206 (2) 231-5.
Journal code: 4NK. ISSN: 0003-2697.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199302
AB We investigated the usefulness of the polymerase chain reaction (PCR) method for the relative quantification of gene expression using a simultaneously amplified sequence of beta-actin mRNA as an internal control for the target sequence of tax/rex mRNA of human T-cell leukemia virus type I. The PCR product of the internal control was reduced by delaying the addition of the primers for its sequence. The photostimulated luminescence of the bands was measured with a laser image analyzer, and the values were plotted against the cycle number. The cycle differences between the logarithmic phase of the curves for the target sequence and for beta-actin (delta cycle) showed a linear correlation with the initial concentration of the sample. This method is highly sensitive for evaluating gene expression over a wide range.

L15 ANSWER 63 OF 74 MEDLINE
AN 92382595 MEDLINE
DN 92382595
TI Development of cell surface protein associated gene probe specific for Listeria monocytogenes and detection of the bacteria in food by PCR.
AU Wang R F; Cao W W; Johnson M G
CS Department of Food Science and Arkansas Biotechnology Center, University of Arkansas, Fayetteville 72703..
SO MOLECULAR AND CELLULAR PROBES, **(1992 Apr)** 6 (2) 119-29.
Journal code: NG9. ISSN: 0890-8508.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199212
AB A genomic library of L. monocytogenes was constructed using lambda Zap II-Eco RI and screened with a monoclonal antibody which is specific for a Listeria cell surface protein. Three positive clones each contained a 6.5 kb insert which in E. coli could express the same Listeria protein. The 6.5 kb insert was further digested with Hin dIII and the smaller fragments were subcloned into a plasmid vector (pBluescript) and screened with 32P-labelled genomic DNA from L. monocytogenes or L. innocua. Three clones

which were positive with L. monocytogenes and negative with L. innocua were screened and each contained a 2.1 kb insert. The 2.1 kb insert was partly sequenced and some candidate **oligomer** probes from the sequences were selected and compared with sequences in a Genbank computer search. One such **oligomer** probe (T7-list) was confirmed to be specific for L. monocytogenes. The probe hybridized with all 28 strains of L. monocytogenes tested, but not with any of six other Listeria species nor 11 other bacteria tested. Using this probe-primer, a PCR method was developed which could detect as few as 2 cfu of L. monocytogenes in pure cultures, and as few as 4-10 cfu of L. monocytogenes when inoculated into foods.

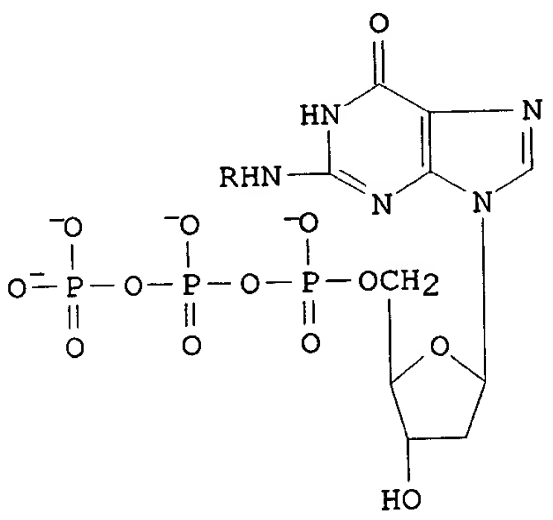
L15 ANSWER 64 OF 74 MEDLINE
AN 95334835 MEDLINE
DN 95334835
TI Preparation of radiolabelled hybridization probes by STS labelling.
AU Hirst M C; Bassett J H; Roche A; Davies K E
CS Institute of Molecular Medicine, John Radcliffe Hospital, Headington, Oxford, UK..
SO TRENDS IN GENETICS, **(1992 Jan)** 8 (1) 6-7.
Journal code: WEK. ISSN: 0168-9525.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
EM 199510

L15 ANSWER 65 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1991:553738 CAPLUS
DN 115:153738
TI Human immunodeficiency virus reverse transcriptase. Effect of primer length on template-primer binding
AU Reardon, John E.; Furfine, Eric S.; Cheng, Nancy
CS Div. Exp. Ther., Wellcome Res. Lab., Research Triangle Park, NC, 27709, USA
SO J. Biol. Chem. **(1991)**, 266(21), 14128-34
CODEN: JBCHA3; ISSN: 0021-9258
DT Journal
LA English
AB Poly(rA).cntdot.**oligo**(dT)n (I) binding to human immunodeficiency virus type-1 (HIV-1) reverse transcriptase (RT) heterodimer (p66-p51) was primer length-dependent. The estd. Kd for I (n = 10-14) was 20-30 nM and for I (n = 16-20) was 0.11-0.14 nM. Gel electrophoretic anal. of the patterns of primer extension was consistent with an abrupt change in the Kd between a primer length of 14 and 16 **nucleotides**. Further, the rate const. for dissocn. of the RT-template-primer complex was detd. from steady state kinetics and enzyme-template-primer trapping expts. to be independent of primer length. Thus, the abrupt change in Kd was most likely due to a change in the rate const. for formation of the RT-template-primer complex. A similar shift in the Kd for template-primer binding was obsd. with poly(dA).cntdot.**oligo**(dT)n. RT homodimer (p66) catalyzed the incorporation of dTMP into I with the same primer length dependence obsd. for the heterodimer. In contrast, the binding of the p51 homodimer to I was independent of primer length. Thus, the RNase H domain may contribute to RT heterodimer or p66 homodimer binding to template-primers in which the primer length is >14 **nucleotides**.

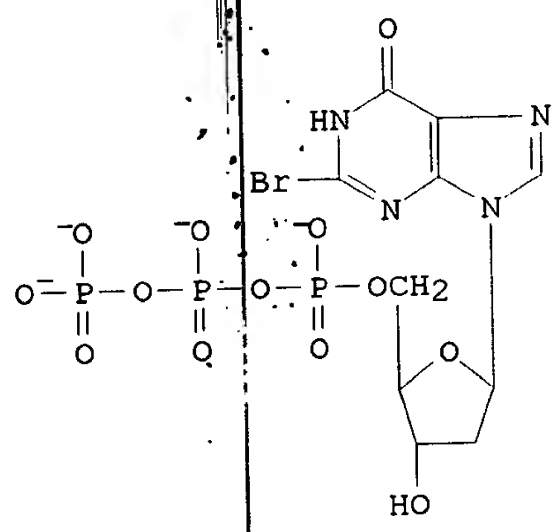
L15 ANSWER 66 OF 74 CAPLUS COPYRIGHT 2000 ACS DUPLICATE 10
AN 1992:36003 CAPLUS
DN 116:36003
TI DNA polymerase-mediated **nucleotide** incorporation adjacent to hydrocarbon-**deoxyadenosine** and hydrocarbon-**deoxyguanosine** adducts
AU Hruszkewycz, Andrew M.; Canella, Karen A.; Dipple, Anthony

CS Frederick Cancer Res. Dev. Cent., NCI, Frederick, MD, 21702, USA
SO Carcinogenesis (London) (**1991**), 12(9), 1659-6
CODEN: CRNGDP; ISSN: 0143-3334
DT Journal
LA English
AB To examine the effect of DNA adducts on **nucleotide** incorporation by DNA polymerase at 3' neighboring bases, synthetic **oligonucleotides** (16mers) contg. a purine at position 13 from the 3' end and any one of the four possible bases at position 12 were prepd. and reacted with 7-bromomethylbenz[a]anthracene. Using HPLC, unmodified **oligonucleotide** was sepd. from **oligonucleotide** contg. a single adduct, at either an adenine or a guanine residue. These products were annealed with a 32P 5'-end-labeled primer (11mer) and incubated with modified T7 DNA polymerase (Sequenase, version 2.0) in the presence of deoxyribonucleoside **5'-triphosphates**. Anal. by gel electrophoresis showed that unmodified **oligonucleotide** template allowed the primer to be rapidly extended to the entire length of the template. However, the presence of an adduct caused primer extension to stop at the base 3' to the adduct. While correct base pairing occurred at this termination site with most adducted templates, there was a high frequency of misincorporation of guanine opposite a thymine located 3' to an adenine adduct. This result suggests that some bulky carcinogen-DNA adducts may lead to base mismatches at neighboring bases.

L15 ANSWER 67 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1992:41953 CAPLUS
DN 116:41953
TI N2-Substituted-2'-**deoxyguanosine 5'-triphosphates** as substrates for E. coli DNA polymerase I
AU Freese, Stephen; Hoheisel, Jorg; Lehrach, Hans; Wright, George
CS Med. Sch., Univ. Massachusetts, Worcester, MA, 01655, USA
SO Nucleosides Nucleotides (**1991**), 10(7), 1507-24
CODEN: NUNUD5; ISSN: 0732-8311
DT Journal
LA English
GI



I



II

AB Several N2-alkyl I [R = Me, Et, CF3CH2, Me(CH2)5] and N2-Ph 2'-**deoxyguanosine 5'-triphosphates** I (R = Ph) and 2-bromo-2'-**deoxyinosine 5'-triphosphate** (II) were synthesized and tested as substrates for E. coli DNA polymerase I with a template:primer system requiring incorporation of 85 **nucleotides**. I (R = Me, Et) were found to be efficiently incorporated in place of dGTP to give full length product. I [R = (CH2)5Me] supported limited full length synthesis at high concn., but I (R

= Ph) and I [R = C6H4(CH2)3Me-p] were poor substrates. II was a good substrate for polymerase I, and it was a replacement only for dGTP. Melting temps. of **oligodeoxyribonucleotides** contg. N2-alkyl-dG residues, annealed to complementary single stranded DNA, were lower than that of the normal **oligomer**.

L15 ANSWER 68 OF 74 MEDLINE
AN 91378993 MEDLINE
DN 91378993
TI The **5'-triphosphates** of 3'-azido-3'-**deoxythymidine** and 2', 3'-dideoxynucleosides inhibit DNA polymerase gamma by different mechanisms.
AU Izuta S; Saneyoshi M; Sakurai T; Suzuki M; Kojima K; Yoshida S
CS Laboratory of Cancer Cell Biology, Nagoya University School of Medicine, Japan..
SO BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, **(1991 Sep 16)** 179 (2) 776-83.
Journal code: 9Y8. ISSN: 0006-291X.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 199112
AB Inhibition mechanisms of **5'-triphosphates** of 3'-azido-3'-**deoxythymidine** (AZT-TP) and 3'-**deoxythymidine** (ddTTP) on extensively purified DNA polymerase gamma from bovine testes were examined by analysis of the products synthesized on singly primed M13 single-stranded DNA or synthetic **oligonucleotide** template-primer in the presence of analogues. The results indicate that AZT-TP inhibits DNA polymerase gamma in competition with dTTP but is not incorporated into DNA, whereas ddTTP is incorporated into DNA and causes chain termination. In contrast, both analogues were used by reverse transcriptase and caused chain termination.

L15 ANSWER 69 OF 74 MEDLINE
AN 91191737 MEDLINE
DN 91191737
TI Evidence for the mutagenic potential of the vinyl chloride induced adduct, N2, 3-etheno-**deoxyguanosine**, using a site-directed kinetic assay.
AU Singer B; Kusmierek J T; Folkman W; Chavez F; Dosanjh M K
CS Donner Laboratory, Lawrence Berkeley Laboratory, University of California, Berkeley 94720.
NC CA 47723 (NCI)
SO CARCINOGENESIS, **(1991 Apr)** 12 (4) 745-7.
Journal code: C9T. ISSN: 0143-3334.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 199107
AB N2,3-Ethenoguanine (epsilon G) is a product of vinyl chloride reaction with DNA in vivo and of its ultimate metabolite, chloroacetaldehyde, in vitro. The synthesis of the very labile **5'-triphosphate** of N2,3-etheno-**deoxyguanosine** (epsilon dGuo) has made it possible to study the base pairing properties of this derivative placed opposite a defined normal base in a 25-base **oligonucleotide** template. The kinetic parameters, Km and Vmax were determined from elongation of a [32P]5'-end labeled primer annealed one base prior to the designated template base, epsilon G.T pairs, which would be mutagenic, were formed with a frequency 2- to 4-fold greater than the analogous wobble pair, G.T. The non-mutagenic pairing, epsilon G.C, occurs with a lower frequency than G.C but neither epsilon G.T or epsilon G.C constitute

a significant block to replication. The frequency of epsilon G.T formation was similar with all polymerases tested: Escherichia coli DNA polymerase I (Klenow fragment), exonuclease-free Klenow, Drosophila melanogaster polymerase alpha-primase complex and human immunodeficient virus-I reverse transcriptase (HIV-RT). It is concluded that these prokaryotic and eukaryotic replicating enzymes apparently recognize the same structural features, and on replication G----A transitions would occur, which in turn, could initiate malignant transformation. In contrast to the G.T mismatch which is known to have a specific repair system, etheno derivatives are apparently not repaired in vivo.

L15 ANSWER 70 OF 74 MEDLINE
AN 91105138 MEDLINE
DN 91105138
TI Effects of 2-chloro-2'-**deoxyadenosine 5'-triphosphate** on DNA synthesis in vitro by purified bacterial and viral DNA polymerases.
AU Hentosh P; McCastlain J C; Blakley R L
CS Department of Biochemical and Clinical Pharmacology, St. Jude Children's Research Hospital, Memphis, Tennessee 38101.
NC RO1 CA 39242 (NCI)
P30 CA 21765 (NCI)
SO BIOCHEMISTRY, **(1991 Jan 15)** 30 (2) 547-54.
Journal code: A0G. ISSN: 0006-2960.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199105
AB 2-Chloro-2'-**deoxyadenosine 5'-triphosphate** (CldATP) was compared with dATP as a substrate for DNA synthesis by bacterial and viral DNA polymerases in vitro. Lengths of chain extension and DNA synthesis pause sites were determined by comparison with products generated by dideoxynucleotide sequencing methods on the same end-labeled primer/template duplex after high-resolution polyacrylamide gel electrophoresis. Reverse transcriptase (RT) from human immunodeficiency virus (HIV-1) and avian myeloblastosis virus (AMV) incorporated CldATP efficiently. DNA strand elongation continued past most chloroadenine (ClA) insertion sites but resulted in shorter chains than when dATP was inserted. Phage T4 DNA polymerase incorporated CldATP least efficiently; Klenow fragment of Escherichia coli DNA polymerase I and modified T7 DNA polymerase (Sequenase) showed intermediate ability to utilize the analogue. Incorporation of several consecutive ClA residues into the replicating strand dramatically reduced the ability of Sequenase, Klenow fragment, and T4 DNA polymerases to continue strand elongation. In the absence of the corresponding normal deoxyribonucleoside triphosphate during DNA synthesis, ClA was frequently misincorporated as thymine, cytosine, or guanine by both AMV RT and HIV-1 RT but rarely, if at all, by Klenow fragment, Sequenase, and T4 DNA polymerase. Except T4, for most DNA polymerases, CldATP at 10-20-fold molar excess over dATP was not a strong competitive inhibitor of dATP, as judged by the amount of strand extension and polymerase pause sites during DNA synthetic reactions. Our results indicate that the degree of strand extension in the presence of CldATP, the number and location of polymerase pause sites, and the amount of misincorporation of the analogue are both polymerase- and sequence-dependent.

L15 ANSWER 71 OF 74 MEDLINE

AN 91243801 MEDLINE
DN 91243801
TI Mutational analysis of two conserved sequence motifs in HIV-1 reverse transcriptase.
AU Lowe D M; Parmar V; Kemp S D; Larder B A
CS Department of Molecular Sciences, Wellcome Research Laboratories, Beckenham, Kent, U.K.
SO FEBS LETTERS, **(1991 May 6)** 282 (2) 231-4.
Journal code: EUH. ISSN: 0014-5793.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 199109
AB Two conserved sequence motifs, occurring in HIV-1 reverse transcriptase at residues 110-116 and 183-190, have been studied using site-directed mutagenesis of the cloned gene. In particular, aspartates at positions 185 and 186 have each been mutated to either asparagine or glutamate. The resulting mutant proteins were catalytically inactive but still able to bind the template-primer complex, poly rA-**oligo** dT. Other mutations in these regions resulted in reduced reverse trascriptase activity but the mutation of tyrosine-183 to serine caused a significant increase in the Km for dTTP and the Ki for inhibition by 3'-azidothymidine-triphosphate, 2',3'-dideoxythymidine-triphosphate and phosphonoformic acid.

L15 ANSWER 72 OF 74 MEDLINE
AN 92160607 MEDLINE
DN 92160607
TI Metabolism and action of 2',2'-difluorodeoxycytidine: self-potentiation of cytotoxicity.
AU Gandhi V; Huang P; Xu Y Z; Heinemann V; Plunkett W
CS Department of Medical Oncology, University of Texas M. D. Anderson Cancer Center, Houston 77030.
NC CA28596 (NCI)
CA53311 (NCI)
SO ADVANCES IN EXPERIMENTAL MEDICINE AND BIOLOGY, **(1991)** 309A 125-30.
Journal code: 2LU. ISSN: 0065-2598.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199205

L15 ANSWER 73 OF 74 CAPLUS COPYRIGHT 2000 ACS
AN 1992:604618 CAPLUS
DN 117:204618
TI Mechanisms of inhibitions of DNA polymerase .gamma. by **nucleotide** analogs having anti-HIV activities
AU Izuta, Shunji; Saneyoshi, Mineo; Sakurai, Takeshi; Suzuki, Motoshi; Kojima, Kiyohide; Yoshida, Shonen
CS Sch. Med., Nagoya Univ., Nagoya, 466, Japan
SO Nucleic Acids Symp. Ser. (**1991**), 25(Symp. Nucleic Acids Chem., 18th, 1991), 79-80
CODEN: NACSD8; ISSN: 0261-3166
DT Journal
LA English
AB Inhibition mechanisms of **5'-triphosphates** of 3'-azido-3'-**deoxythymidine** (AZT-TP) and 3'-**deoxythymidine** (ddTTP) on extensively purified DNA polymerase .gamma. from bovine testes were examd. by anal. of the products

synthesized on singly primed M13mp18 single-stranded DNA or synthetic **oligonucleotide** template-primer in the presence of analogs. The results indicate that AZT-TP inhibits DNA polymerase .gamma. in competition with dTTP but is not incorporated into DNA, whereas ddTTP is incorporated into DNA and causes chain termination.

L15 ANSWER 74 OF 74 MEDLINE
AN 93065322 MEDLINE
DN 93065322
TI Mechanisms of inhibitions of DNA polymerase gamma by **nucleotide** analogues having anti-HIV activities.
AU Izuta S; Saneyoshi M; Sakurai T; Suzuki M; Kojima K; Yoshida S
CS Laboratory of Cancer Cell Biology, Nagoya University School of Medicine, Japan.
SO NUCLEIC ACIDS SYMPOSIUM SERIES, **(1991)** (25) 79-80.
Journal code: O8N. ISSN: 0261-3166.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199302
AB Inhibition mechanisms of **5'-triphosphates** of 3'-azido-3'-**deoxythymidine** (AZT-TP) and 3'-**deoxythymidine** (ddTTP) on extensively purified DNA polymerase gamma from bovine testes were examined by analysis of the products synthesized on singly primed M13mp18 single-stranded DNA or synthetic **oligonucleotide** template-primer in the presence of analogues. The results indicate that AZT-TP inhibits DNA polymerase gamma in competition with dTTP but is not incorporated into DNA, whereas ddTTP is incorporated into DNA and causes chain termination.

```
 e au=sampson, jeffrey

Ref    Items  Index-term
E1         2  AU=SAMPSON-STROMAN V
E2         4  AU=SAMPSON-WARD L
E3         0 *AU=SAMPSON, JEFFREY
E4         1  AU=SAMPSONIDIS D
E5         1  AU=SAMPT ER
E6         2  AU=SAMPTIAUX P
E7        98  AU=SAMPUGNA J
E8         6  AU=SAMPUGNA JOSEPH
E9         2  AU=SAMPUGNARO V
E10        1  AU=SAMPURNANAND C
E11        1  AU=SAMPURNO B
E12        1  AU=SAMPURNO S B

          Enter P or PAGE for more
? e au=sampson jeffrey

Ref    Items  Index-term
E1         2  AU=SAMPSON JE
E2         4  AU=SAMPSON JEFF
E3         0 *AU=SAMPSON JEFFREY
E4         7  AU=SAMPSON JEFFREY R
E5         1  AU=SAMPSON JENNIFER R
E6         1  AU=SAMPSON JF
E7        32  AU=SAMPSON JH
E8         1  AU=SAMPSON JILL
E9        12  AU=SAMPSON JJ
E10        1  AU=SAMPSON JM
E11        1  AU=SAMPSON JO-ANN
E12       15  AU=SAMPSON JOHN H

          Enter P or PAGE for more
? s e2 or e4

               4  AU=SAMPSON JEFF
               7  AU=SAMPSON JEFFREY R
      S1      11  AU="SAMPSON JEFF" OR AU="SAMPSON JEFFREY R"
? rd

...completed examining records
      S2      11  RD (unique items)
? t s2/3,ab/all


 2/3,AB/1     (Item 1 from file: 5)
DIALOG(R)File   5:Biosis Previews(R)
(c) 2000 BIOSIS. All rts. reserv.

11398575   BIOSIS NO.: 199800179907
Evolution of a transfer RNA gene through a point mutation in the anticodon.
AUTHOR: Saks Margaret E(a); Sampson Jeffrey R; Abelson Joh
AUTHOR ADDRESS: (a)Dep. Biol., Univ. Oregon, Eugene, OR 97403**USA
1998
JOURNAL: Science (Washington D C)  279 (5357):p1665-1670 March 13, 1998
ISSN: 0036-8075
```

DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The transfer RNA (tRNA) multigene family comprises 20 amino acid-accepting groups, many of which contain isoacceptors. The addition of isoacceptors to the tRNA repertoire was critical to establishing the genetic code, yet the origin of isoacceptors remains largely unexplored. A model of tRNA evolution, termed "tRNA gene recruitment," was formulated. It proposes that a tRNA gene can be recruited from one isoaccepting group to another by a point mutation that concurrently changes tRNA amino acid identity and messenger RNA coupling capacity. A test of the model showed that an Escherichia coli strain, in which the essential tRNAUGUThr gene was inactivated, was rendered viable when a tRNAArg with a point mutation that changed its anticodon from UCU to UGU (threonine) was expressed. Insertion of threonine at threonine codons by the "recruited" tRNAArg was corroborated by in vitro aminoacylation assays showing that its specificity had been changed from arginine to threonine. Therefore, the recruitment model may account for the evolution of some tRNA genes.

2/3,AB/2 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

10850583 BIOSIS NO.: 199799471728
Variability of canine microsatellites within and between different dog breeds.
AUTHOR: Zajc Irena(a); Mellersh Cathryn S; **Sampson Jeff**
AUTHOR ADDRESS: (a)Natl. Inst. Biol., Karlovska 19, 1000 Ljubljana** Slovenia
1997
JOURNAL: Mammalian Genome 8 (3):p182-185 1997
ISSN: 0938-8990
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Polymorphic animal mictosatellites have proved valuable genetic markers. For this project, the variability of 19 canine microsatellite loci was examined within and between three pure breeds of dog: Greyhounds, Labradors, and German Shepherds. The number of alleles, absolute and relative frequencies, and the statistics that express polymorphism within a breed were determined. The evolutionary relationships among these closely related dog breeds were estimated by genetic distance measures developed for use with microsatellite loci. According to the pairwise genetic distances, Greyhounds and German Shepherds had longer diverse evolutionary histories than Greyhounds and Labradors or Labradors and German Shepherds. Although a few breed-specific alleles were observed, the significant differences between breeds are in their relative frequencies and distribution of the alleles across a locus. None of the three pure dog breeds corresponds to Hardy-Weinberg equilibrium. A considerable reduction in intrapopulation variation was observed within three pure breeds, compared with the population of individuals belonging to 15 dog breeds. This reduction was especially pronounced in the Greyhound breed, which expressed the lowest degree of variation. Intrapopulation variations of Labradors and German Shepherds did not differ significantly, that of Labradors being only slightly higher. The intraspecies variation of dogs is lower than in humans, mouse, or rat, but similar to that in domestic animals, probably reflecting similarly high inbreeding coefficients. However, some highly informative loci were common to all dog breeds tested so far. Such population data are necessary for mapping studies and linkage analysis in dogs.

2/3,AB/3 (Item 3 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2000 BIOSIS. All rts. reserv.

10604389 BIOSIS NO.: 199699225534
An engineered Tetrahymena tRNA-Gln for in vivo incorporation of unnatural amino acids into proteins by nonsense suppression.
AUTHOR: Saks Margaret E; **Sampson Jeffrey R**; Nowek Mark W; Kearney Patrick C; Du Fangyong; Abelson John N; Lester Henry A; Dougherty Dennis A(a
AUTHOR ADDRESS: (a)Div. Chem. and Chem. Eng. 164-30, Calif. Inst. Technol., Pasadena, CA 91125**USA
1996
JOURNAL: Journal of Biological Chemistry 271 (38):p23169-23175 1996
ISSN: 0021-9258
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: A new tRNA, THG73, has been designed and evaluated as a vehicle for incorporating unnatural amino acids site-specifically into proteins expressed in vivo using the stop codon suppression technique. The construct is a modification of tRNA-Glu(CUA) from Tetrahymena thermophila, which naturally recognizes the stop codon UAG. Using electrophysiological studies of mutations at several sites of the nicotinic acetylcholine receptor, it is established that THG73 represents a major improvement over previous nonsense suppressors both in terms of efficiency and fidelity of unnatural amino acid incorporation. Compared with a previous tRNA used for in vivo suppression, THG73 is as much as 100-fold less likely to be acylated by endogenous synthetases of the Xenopus oocyte. This effectively eliminates a major concern of the in vivo suppression methodology, the undesirable incorporation of natural amino acids at the suppression site. In addition, THG73 is 4-10-fold more efficient at incorporating unnatural amino acids in the oocyte system. Taken together, these two advances should greatly expand the range of applicability of the in vivo nonsense suppression methodology.

2/3,AB/4 (Item 4 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2000 BIOSIS. All rts. reserv.

10453877 BIOSIS NO.: 199699075022
DNA microsatellites in domesticated dogs: Application in paternity disputes.
AUTHOR: Zajc Irena(a); **Sampson Jeff**
AUTHOR ADDRESS: (a)National Inst. Biol., Karlovska 19, SI-61000 Ljubljana** Slovenia
1996
JOURNAL: Pfluegers Archiv European Journal of Physiology 431 (6 SUPPL. 2): pR201-R202 1996
CONFERENCE/MEETING: International Meeting: Life Sciences 1995 Gzod Martuljek, Slovenia September 23-28, 1995
ISSN: 0031-6768
RECORD TYPE: Citation
LANGUAGE: English

2/3,AB/5 (Item 5 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)
(c) 2000 BIOSIS. All rts. reserv.

10439678 BIOSIS NO.: 199699060823
Variant minihelix RNAs reveal sequence-specific recognition of the helical

tRNA-Ser acceptor stem by E. coli seryl-tRNA synthetase.
AUTHOR: Saks Margaret E; **Sampson Jeffrey R**
AUTHOR ADDRESS: Div. Biology, 147-74, Calif. Inst. Technol., Pasadena, CA 91125**USA
1996
JOURNAL: EMBO (European Molecular Biology Organization) Journal 15 (11):p 2843-2849 1996
ISSN: 0261-4189
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Aminoacylation rate determinations for a series of variant RNA minihelix substrates revealed that Escherichia coli seryl-tRNA synthetase (SerRS) recognizes the 1-72 through 5-68 base pairs of the E. coli tRNA-Ser acceptor stem with the major recognition elements clustered between positions 2-71 and 4-69. The rank order of effects of canonical base pair substitutions at each position on k-cat/K-m was used to assess the involvement of major groove functional groups in recognition. Conclusions based on the biochemical data are largely consistent with the interactions revealed by the refined structure of the homologous Thermus thermophilus tRNA-Ser-SerRS complex that Cusack and colleagues report in the accompanying paper. Disruption of an end-on hydrophobic interaction between the major groove C5(H) of pyrimidine 69 and an aromatic side chain of SerRS is shown to significantly decrease k-cat/K-m of a minihelix substrate. This type of interaction provides a means by which proteins can recognize the binary information of 'degenerate' sequences, such as the purine-pyrimidine base pairs of tRNA-Ser. The 370 base pair is shown to contribute to recognition by SerRS even though it is not contacted specifically by the protein. The latter effect derives from the organization of the specific contacts that SerRS makes with the neighboring 2-71 and 4-69 acceptor stem base pairs.

2/3,AB/6 (Item 6 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

09857256 BIOSIS NO.: 199598312174
Evolution of tRNA recognition systems and tRNA gene sequences.
AUTHOR: Saks Margaret E(a); **Sampson Jeffrey R**
AUTHOR ADDRESS: (a)Div. Biol. 147-75, Calif. Inst. Technol., Pasadena, CA 91125**USA
1995
JOURNAL: Journal of Molecular Evolution 40 (5):p509-518 1995
ISSN: 0022-2844
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The aminoacylation of tRNAs by the aminoacyl-tRNA synthetases recapitulates the genetic code by dictating the association between amino acids and tRNA anticodons. The sequences of tRNAs were analyzed to investigate the nature of primordial recognition systems and to make inferences about the evolution of tRNA gene sequences and the evolution of the genetic code. Evidence is presented that primordial synthetases recognized acceptor stem nucleotides prior to the establishment of the three major phylogenetic lineages. However, acceptor stem sequences probably did not achieve a level of sequence diversity sufficient to faithfully specify the anticodon assignments of all 20 amino acids. This putative bottleneck in the evolution of the genetic code may have been alleviated by the advent of anticodon recognition. A phylogenetic analysis of tRNA gene sequences from the deep Archaea revealed groups that are united by sequence motifs which are located within a region of the tRNA that is involved in determining its tertiary structure. An

association between the third anticodon nucleotide (N36) and these sequence motifs suggests that a tRNA-like structure existed close to the time that amino acid-anticodon assignments were being established. The sequence analysis also revealed that tRNA genes may evolve by anticodon mutations that recruit tRNAs from one isoaccepting group to another. Thus tRNA gene evolution may not always be monophyletic with respect to each isoaccepting group.

2/3,AB/7 (Item 7 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

09823089 BIOSIS NO.: 199598278007
Nicotinic receptor binding site probed with unnatural amino acid incorporation in intact cells.
AUTHOR: Nowak Mark W; Kearney Patrick C; **Sampson Jeffrey R**; Saks Margaret E; Labarca Cesar G; Silverman Scott K; Zhong Wenge; Thorson Jon; Abelson John N; Davidson Norman; Schultz Peter G; Dougherty Dennis A; Lester Henry A(a
AUTHOR ADDRESS: (a)Div. Biol., California Inst. Technology, Pasadena, CA 91125**USA
1995
JOURNAL: Science (Washington D C) 268 (5209):p439-442 1995
ISSN: 0036-8075
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The nonsense codon suppression method for unnatural amino acid incorporation has been applied to intact cells and combined with electrophysiological analysis to probe structure-function relations in the nicotinic acetylcholine receptor. Functional receptors were expressed in Xenopus oocytes when tyrosine and phenylalanine derivatives were incorporated at positions 93, 190, and 198 in the binding site of the alpha subunit. Subtle changes in the structure of an individual side chain produced readily detectable changes in the function of this large channel protein. At each position, distinct features of side chain structure dominated the dose-response relation, probably by governing the agonist-receptor binding.

2/3,AB/8 (Item 8 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

09125977 BIOSIS NO.: 199497134347
Simplifying detection of microsatellite length polymorphisms.
AUTHOR: Mellersh Cathryn(a); **Sampson Jeff**
AUTHOR ADDRESS: (a)Dep. Biochem., Univ. Leicester, University Rd., Leicester LE1 7RH**UK
1993
JOURNAL: Biotechniques 15 (4):p582, 584 1993
ISSN: 0736-6205
DOCUMENT TYPE: Article
RECORD TYPE: Citation
LANGUAGE: English

2/3,AB/9 (Item 9 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

09114098 BIOSIS NO.: 199497122468
The transfer RNA identity problem: A search for rules.

AUTHOR: Saks Margaret E(a); **Sampson Jeffrey R**(a); Abelson John N
AUTHOR ADDRESS: (a)Div. Biol., Calif. Inst. Tech., Pasadena, CA 91125**
USA
1994
JOURNAL: Science (Washington D C) 263 (5144):p191-197 1994
ISSN: 0036-8075
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Correct recognition of transfer RNAs (tRNAs) by aminoacyl-tRNA synthetases is central to the maintenance of translational fidelity. The hypothesis that synthetases recognize anticodon nucleotides was proposed in 1964 and had considerable experimental support by the mid-1970s. Nevertheless, the idea was not widely accepted until relatively recently in part because the methodologies initially available for examining tRNA recognition proved hampering for adequately testing alternative hypotheses. Implementation of new technologies has led to a reasonably complete picture of how tRNAs are recognized. The anticodon is indeed important for 17 of the 20 Escherichia coli isoaccepting groups. For many of the isoaccepting groups, the acceptor stem or position 73 (or both) is important as well.

2/3,AB/10 (Item 10 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

08996013 BIOSIS NO.: 199497004383
Contributions of discrete tRNA-Ser domains to amino-acylation by E. coli seryl-tRNA synthetase: A kinetic analysis using model RNA substrates.
AUTHOR: **Sampson Jeffrey R**; Saks Margaret E
AUTHOR ADDRESS: Div. Biol. 147-75, Calif. Inst. Technol., Pasadena, CA 91125**USA
1993
JOURNAL: Nucleic Acids Research 21 (19):p4467-4475 1993
ISSN: 0305-1048
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: The aminoacylation kinetics of T7 transcripts representing defined regions of Escherichia coli serine tRNAs were determined using purified E. coli seryl-tRNA synthetase (SerRS) and the kinetic values were used to estimate the relative contribution of various tRNA-Ser domains to recognition by SerRS. The analysis revealed that the extra stem/loop structure, characteristic of type II tRNAs such as tRNA-Ser, is the domain which makes the largest contribution to k-cat/K-m of aminoacylation. Moreover, K-m of aminoacylation was increased by a factor of about 1000 when the extra stem/loop was changed to the consensus sequence of type I tRNA extra loops indicating that the stem structure contributes significantly to the binding of tRNA-Ser to SerRS. A model RNA, which represents only the tRNAser coaxial acceptor-T-psi-C stem/loop domain, was also specifically aminoacylated by SerRS having a k-cat/K-m about 1000-fold greater than background levels. A significant portion of the contribution of this domain to aminoacylation is attributable to the acceptor stem sequence making the acceptor stem the second most important domain for recognition by SerRS. Finally, K-cat/K-m was essentially unchanged when the entire anticodon stem/loop of tRNA-Ser was deleted indicating that neither the anticodon nucleotides nor the surrounding stem/loop structure are important for recognition by SerRS.

2/3,AB/11 (Item 11 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

08540542 BIOSIS NO.: 199344090542
Enhancing understanding of recombinant DNA technology.
AUTHOR: Harrison Jennifer(a); **Sampson Jeff**; Harrison Tim
AUTHOR ADDRESS: (a)Sch. Educ., Univ. Leicester, 21 University Road, Leicester LE1 7RF
1992
JOURNAL: Journal of Biological Education 26 (4):p300-306 1992
ISSN: 0021-9266
DOCUMENT TYPE: Article
RECORD TYPE: Citation

```
     ---  -----  ----------
? s hydrogen? (w) bond?

          280094  HYDROGEN?
          129958  BOND?
      S1   29029  HYDROGEN? (W) BOND?
? s s1 and nucleic (w) acid

           29029  S1
          174330  NUCLEIC
         1938997  ACID
          154298  NUCLEIC(W)ACID
      S2    2902  S1 AND NUCLEIC (W) ACID
? s s1 and nucleic (w) acid?

           29029  S1
          174330  NUCLEIC
         2330373  ACID?
          173568  NUCLEIC(W)ACID?
      S3    3086  S1 AND NUCLEIC (W) ACID?
? s s3 and ?structur?

>>>File 155 processing for ?STRUCTUR? stopped at AMADEN
>>>File 5 processing for ?STRUCTUR? stopped at AC3F
             3086  S3
                0  ?STRUCTUR?
      S4        0  S3 AND ?STRUCTUR?
? s s3 and una

             3086  S3
            13270  UNA
      S5        0  S3 AND UNA
? s s3 and modif?

             3086  S3
           526689  MODIF?
      S6     336  S3 AND MODIF?
? rd

...examined 50 records  (50)
...examined 50 records  (100)
...examined 50 records  (150)
...examined 50 records  (200)
...examined 50 records  (250)
...examined 50 records  (300)
...completed examining records
      S7     312  RD (unique items)
? s s7 and base?

              312  S7
          1448258  BASE?
      S8      271  S7 AND BASE?
? s s8 and intramolec?

              271  S8
            18988  INTRAMOLEC?
      S9       11  S8 AND INTRAMOLEC?
? s s8 and complement?
```

```
            271  S8
          35173  COMPLEMENT?
     S10       45  S8 AND COMPLEMENT?
? s s10 not s9

               45  S10
               11  S9
     S11       43  S10 NOT S9
? t s9/3,ab/all and s10/3,ab/all

>>>'AND' not allowed in command
? t s9/3,ab/all
```

9/3,AB/1 (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
(c) format only 2000 Dialog Corporation. All rts. reserv.

10432880 20303411
A perspective of biological supramolecular electron transfer.
Ramasarma T
Department of Biochemistry, Indian Institute of Science, Bangalore. trs@biochem.iisc.ernet.in
Indian journal of biochemistry & biophysics (INDIA) Dec 1999, 36 (6) p379-97, ISSN 0301-1208 Journal Code: GHW
Languages: ENGLISH
Document type: JOURNAL ARTICLE

Electron transfer is an essential activity in biological systems. The migrating electron originates from water-oxygen in photosynthesis and reverts to dioxygen in respiration. In this cycle two metal porphyrin complexes possessing circular conjugated system and macrocyclic pi-clouds, chlorophyll and heme, play a decisive role in mobilising electrons for travel over biological structures as extraneous electrons. Transport of electrons within proteins (as in cytochromes) and within DNA (during oxidative damage and repair) is known to occur. Initial evaluations did not favour formation of semiconducting pathways of delocalized electrons of the peptide bonds in proteins and of the **bases** in **nucleic acids** . Direct measurement of conductivity of bulk material and quantum chemical calculations of their polymeric structures also did not support electron transfer in both proteins and **nucleic acids**.
New experimental approaches have revived interest in the process of charge transfer through DNA duplex. The fluorescence on photo-excitation of Ru-complex was found to be quenched by Rh-complex, when both were tethered to DNA and intercalated in the **base** stack. Similar experiments showed that damage to G-**bases** and repair of T-T dimers in DNA can occur by possible long range electron transfer through the **base** stack. The novelty of this phenomenon prompted the apt name, "chemistry at a distance". **Based** on experiments with ruthenium **modified** proteins, **intramolecular** electron transfer in proteins is now proposed to use pathways that include C-C sigma-bonds and surprisingly **hydrogen bonds** which remained out of favour for a long time. In support of this, some experimental evidence is now available showing that **hydrogen bond**-bridges facilitate transfer of electrons between metal-porphyrin complexes. By molecular orbital calculations over 20 years ago we found that "delocalization of an extraneous electron is pronounced when it enters low-lying virtual orbitals of the electronic structures of peptide units linked by **hydrogen bonds**". This review focuses on supramolecular electron transfer pathways that can emerge on interlinking by **hydrogen bonds** and metal coordination of some unnoticed structures with pi-clouds in proteins and **nucleic acids**, potentially useful in catalysis and energy missions.

9/3,AB/2 (Item 2 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

09773558 99119199

Dual recognition of double-stranded DNA by 2'-aminoethoxy-**modified** oligonucleotides: the solution structure of an **intramolecular** triplex obtained by NMR spectroscopy.

Blommers MJ; Natt F; Jahnke W; Cuenoud B

Core Technologies, Novartis Pharma AG, Basel, Switzerland.

Biochemistry (UNITED STATES) Dec 22 1998, 37 (51) p17714-25, ISSN 0006-2960 Journal Code: A0G

Languages: ENGLISH

Document type: JOURNAL ARTICLE

The solution structure of an **intramolecular** triple helical oligonucleotide has been solved by NMR. The third strand of the pyrimidine x purine x pyrimidine triplex is composed of 2'-aminoethoxy-**modified** riboses, whereas the remaining part of the **nucleic acid** is DNA. The structure around the aminoethoxy **modification** was obtained with the help of selective isotope labeling in conjunction with isotope-editing experiments. Dinucleotide steps and interstrand connectivities, as well as the complete backbone conformation of the triplex, were derived from J-couplings, NOEs, and 31P chemical shifts. The structure of this triplex, solved by distance geometry, explains the extraordinary stability and increase in rate of triplex formation induced by 2'-aminoethoxy-**modified** oligonucleotides: apart from the formation of seven **base** triples, a well-defined **hydrogen-bonding** network is formed across the Crick-Hoogsteen groove involving the amino protons of the aminoethoxy moieties and the phosphates of the purine strand of the DNA. The **modified** strand adopts a conformation which is close to an A-type helix, whereas the DNA duplex conformation is best described as an unwound B-type helix. The groove dimensions and helical parameters of the 2'-aminoethoxy-**modified** rY x dRdY triplex are surprisingly well conserved in comparison with DNA triplexes.

9/3,AB/3 (Item 3 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

08239278 95127702

Solution conformation of the (-)-trans-anti-benzo[c]phenanthrene-dA ([BPh]dA) adduct opposite dT in a DNA duplex: intercalation of the covalently attached benzo[c]phenanthrenyl ring to the 3'-side of the adduct site and comparison with the (+)-trans-anti-[BPh]dA opposite dT stereoisomer.

Cosman M; Laryea A; Fiala R; Hingerty BE; Amin S; Geacintov NE; Broyde S; Patel DJ

Cellular Biochemistry and Biophysics Program, Memorial Sloan-Kettering Cancer Center, New York, New York 10021.

Biochemistry (UNITED STATES) Jan 31 1995, 34 (4) p1295-307, ISSN 0006-2960 Journal Code: A0G

Contract/Grant No.: CA-46533, CA, NCI; CA-20851, CA, NCI; CA-28038, CA, NCI; +

Languages: ENGLISH

Document type: JOURNAL ARTICLE

This paper reports on NMR-molecular mechanics structural studies of the (-)- trans-anti-benzo[c]phenanthrene-dA adduct positioned opposite dT in the sequence context of the d(C1-T2-C3-T4-C5-[BPh]A6-C7-T8-T9-C10-C11).d(G12- G13-A14-A15-G16-T17-G18-A19-G20-A21- G22) duplex (designated as the (-)-trans-anti-[BPh]dA.dT 11-mer duplex). This adduct is derived from the covalent binding of (-)-1,2-dihydroxy-3,4-epoxy-1,2,3,4-tetrahydro-benzo[c] phenanthrene [(-)-anti-BPhDE] to N6 of dA6 in this duplex sequence. The benzo[c]phenanthrenyl and **nucleic acid** exchangeable and nonexchangeable protons were assigned in the predominant conformation following analysis of two-dimensional NMR data sets in H2O and D2O buffer solution. The solution structure of the (-)-trans-anti-[BPh]dA.dT 11-mer

duplex has been determined by incorporating **intramolecular** and carcinogen-DNA proton-proton distances defined by lower and upper bounds deduced from NOESY data sets as restraints in molecular mechanics computations in torsion angle space. The results show that the [BPh]dA6.dT17 **base** pair propeller twists and buckles slightly to permit the covalently attached benzo[c]phenanthrenyl ring to intercalate between the [BPh]dA6.dT17 and dC7.dG16 **base** pairs to the 3'-side of the [BPh]dA6 lesion site without disrupting the Watson-Crick **hydrogen bond** alignments in the **modified** duplex. The strain in the highly sterically hindered fjord region of the benzo[c]phenanthrenyl moiety is relieved by the propeller-like nonplanar geometry of the aromatic phenanthrenyl ring system, which stacks predominantly with the dG16 and dT17 **bases** on the unmodified strand. The benzylic ring adopts a distorted half-chair form, in which the H1 and H2 protons are pseudo-diequatorial and the H3 and H4 protons are pseudodiaxial. The current observation that the (-)-trans-anti-[BPh]dA positioned opposite dT intercalates to the 3'-side of the intact **modified base** pair contrasts with our previous demonstration that the stereoisomeric (+)-trans-anti-[BPh]dA adduct positioned opposite dT intercalates to the 5'-side of the intact **modified base** pair [Cosman, M., et al. (1993b) Biochemistry 32, 12488-12497]. These stereochemically induced structural differences between isomeric [BPh]dA lesions derived from the binding of chiral (+)- and (-)-anti-BPhDE enantiomers may in turn profoundly influence the interactions of the carcinogen-**modified** DNA with repair and replication enzymes in the cell.

9/3,AB/4 (Item 4 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07626029 93181161
Protonated pyrimidine-purine-purine triplex.
Malkov VA; Voloshin ON; Veselkov AG; Rostapshov VM; Jansen I; Soyfer VN; Frank-Kamenetskii MD
Institute of Molecular Genetics, Russian Academy of Science, Moscow.
Nucleic acids research (ENGLAND) Jan 11 1993, 21 (1) p105-11, ISSN 0305-1048 Journal Code: O8L
Contract/Grant No.: GM44700-02, GM, NIGMS
Languages: ENGLISH
Document type: JOURNAL ARTICLE
We have studied a protonated pyrimidine-purine-purine (Py-Pu-Pu) triplex, which is formed between the d(C)nd(G)n duplex and the d(AG)m oligonucleotide as the third strand and carries the CG*A+ protonated **base** -triads. We have observed such an intermolecular complex between a plasmid carrying the d(C)18 d(G)18 insert and the d(AG)5 oligonucleotide without bivalent cations in 200 mM of Na+ at pH4.0. Bivalent cations additionally stabilize the complex. We propose the structures for nearly isomorphous **base** -triads TA*A, CG*G and 'CG*A+. To identify the H-DNA-like structure, which includes the triplex between d(C)n d(G)n duplex and the AG-strand, we have cloned in a superhelical plasmid the insert: G10TTAA(AG)5. The data on photofootprinting and chemical **modification** with diethyl pyrocarbonate, potassium permanganate and dimethyl sulfate demonstrate that the H-like structure with triplex carrying CG*G and CG*A+ **base** triads is actually formed under acid conditions. In the course of this study we have come across unexpected results on probing of Py-Pu-Pu triplexes by dimethyl sulfate (DMS): the protection effect is observed not only for guanines entering the duplex but also for guanines in the third strand lying in the major groove. We have demonstrated this effect not only for the case the novel protonated Py-Pu-Pu triplex but also for the traditional non-protonated Py-Pu-Pu **intramolecular** triplex (H*-DNA) formed by the d(C)37 d(G)37 insert in supercoiled plasmid in the presence of Mg2+ ions.

9/3,AB/5 (Item 5 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07533937 93237220

Solution conformation of the (+)-cis-anti-[BP]dG adduct in a DNA duplex: intercalation of the covalently attached benzo[a]pyrenyl ring into the helix and displacement of the **modified** deoxyguanosine.

Cosman M; de los Santos C; Fiala R; Hingerty BE; Ibanez V; Luna E; Harvey R; Geacintov NE; Broyde S; Patel DJ

Department of Biochemistry and Molecular Biophysics, College of Physicians and Surgeons, Columbia University, New York, New York 10032.

Biochemistry (UNITED STATES) Apr 27 1993, 32 (16) p4145-55, ISSN 0006-2960 Journal Code: A0G

Contract/Grant No.: CA-46533, CA, NCI; CA-21111, CA, NCI; CA-09503, CA, NCI; +

Languages: ENGLISH

Document type: JOURNAL ARTICLE

This paper reports on the solution structure of the (+)-cis-anti-[BP]dG adduct positioned opposite dC in a DNA oligomer duplex which provides the first experimentally **based** solution structure of an intercalative complex of a polycyclic aromatic hydrocarbon covalently bound to the N2 of deoxyguanosine. The combined NMR-energy minimization computation studies were undertaken on the (+)-cis-anti-[BP]dG adduct embedded in the same d(C5-[BP]G6-C7).d(G16-C17-G18) trinucleotide segment of the complementary 11-mer duplex studied previously with the stereoisomeric trans adducts. The exchangeable and nonexchangeable protons of the benzo[a]pyrenyl moiety and the **nucleic acid** were assigned following analysis of two-dimensional NMR data sets in H2O and D2O solution. The solution structure of the (+)-cis-anti-[BP]dG-dC 11-mer duplex has been determined by incorporating **intramolecular** and intermolecular proton-proton distances defined by upper and lower bounds deduced from NOESY data sets as restraints in energy minimization computations. The benzo[a]pyrene ring of [BP]dG6 is intercalated between intact Watson-Crick dC5.dG18 and dC7.dG16 **base** pairs in a right-handed DNA helix. The benzylic ring is in the minor groove while the pyrenyl ring stacks with flanking dC5 and dC7 **bases** on the same strand. The deoxyguanosine ring of [BP]dG6 is not Watson-Crick **base** paired but displaced into the minor groove with its plane parallel to the helix axis and stacks over the sugar ring of dC5. The dC17 **base** on the partner strand is displaced from the center of the helix toward the major groove by the intercalated benzo[a]pyrene ring. This intercalative structure of the (+)-cis-anti-[BP]dG-dC 11-mer duplex exhibits several unusually shifted proton resonances which can be readily accounted for by the ring current contributions of the deoxyguanosine and pyrenyl rings of the [BP]dG6 adduct. Several phosphorus resonances are shifted to low and high field of the unperturbed phosphorus spectral region and have been assigned to internucleotide phosphates centered about the [BP]dG6 **modification** site. These studies define the changes in the helix at the central trinucleotide segment needed to generate the intercalation site for the covalently bound (+)-cis-anti-[BP]dG adduct.(ABSTRACT TRUNCATED AT 400 WORDS)

9/3,AB/6 (Item 6 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07418839 91307670

Conformational preferences of **modified nucleic acid bases** N6-methyl-N6-(N-threonylcarbonyl) adenine and 2-methylthio-N6-(N-threonylcarbonyl) adenine by the quantum chemical PCILO calculations.

Tewari R

Physical Chemistry Division, National Chemical Laboratory, Pune, India.

Journal of biomolecular structure & dynamics (UNITED STATES) Dec 1990, 8 (3) p675-86, ISSN 0739-1102 Journal Code: AH2

Languages: ENGLISH
Document type: JOURNAL ARTICLE
Conformational preferences of the hypermodified **nucleic acid bases** N6-methyl-N6-(N-threonylcarbonyl) Adenine, m6tc6 Ade, and 2-methylthio-N6-(N-threonylcarbonyl) Adenine, mS2 tc6 Ade, have been studied theoretically using the quantum chemical PCILO (Perturbative Configuration Interaction using Localized Orbitals) method. The multidimensional conformational space has been searched using selected grid points formed by combining the various torsion angles which take the favoured values obtained from energy variation with respect to each torsion angle individually. In m6 tc6 Ade and mS 2tc6 Ade alike the threonylcarbonyl substituent preferably orients away (distal) from the imidazole moiety of the adenine ring. And as in the simpler N6-(N-threonylcarbonyl) Adenine, tc6 Ade, the atoms in the ureido group as well as the amino acid carbon atoms C(12) and C(
<------User Break------>
u!
? ds

Set	Items	Description
S1	29029	HYDROGEN? (W) BOND?
S2	2902	S1 AND NUCLEIC (W) ACID
S3	3086	S1 AND NUCLEIC (W) ACID?
S4	0	S3 AND ?STRUCTUR?
S5	0	S3 AND UNA
S6	336	S3 AND MODIF?
S7	312	RD (unique items)
S8	271	S7 AND BASE?
S9	11	S8 AND INTRAMOLEC?
S10	45	S8 AND COMPLEMENT?
S11	43	S10 NOT S9

? t s9/3,ab/all

9/3,AB/1 (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

10432880 20303411
A perspective of biological supramolecular electron transfer.
Ramasarma T
Department of Biochemistry, Indian Institute of Science, Bangalore. trs@biochem.iisc.ernet.in
Indian journal of biochemistry & biophysics (INDIA) Dec 1999, 36 (6) p379-97, ISSN 0301-1208 Journal Code: GHW
Languages: ENGLISH
Document type: JOURNAL ARTICLE
Electron transfer is an essential activity in biological systems. The migrating electron originates from water-oxygen in photosynthesis and reverts to dioxygen in respiration. In this cycle two metal porphyrin complexes possessing circular conjugated system and macrocyclic pi-clouds, chlorophyll and heme, play a decisive role in mobilising electrons for travel over biological structures as extraneous electrons. Transport of electrons within proteins (as in cytochromes) and within DNA (during oxidative damage and repair) is known to occur. Initial evaluations did not favour formation of semiconducting pathways of delocalized electrons of the peptide bonds in proteins and of the **bases** in **nucleic acids** . Direct measurement of conductivity of bulk material and quantum chemical calculations of their polymeric structures also did not support electron transfer in both proteins and **nucleic acids**.
New experimental approaches have revived interest in the process of charge transfer through DNA duplex. The fluorescence on photo-excitation of Ru-complex was found to be quenched by Rh-complex, when both were tethered to DNA and intercalated in the **base** stack. Similar experiments showed

that damage to G-**bases** and repair of T-T dimers in DNA can occur by possible long range electron transfer through the **base** stack. The novelty of this phenomenon prompted the apt name, "chemistry at a distance". **Based** on experiments with ruthenium **modified** proteins, **intramolecular** electron transfer in proteins is now proposed to use pathways that include C-C sigma-bonds and surprisingly **hydrogen bonds** which remained out of favour for a long time. In support of this, some experimental evidence is now available showing that **hydrogen bond**-bridges facilitate transfer of electrons between metal-porphyrin complexes. By molecular orbital calculations over 20 years ago we found that "delocalization of an extraneous electron is pronounced when it enters low-lying virtual orbitals of the electronic structures of peptide units linked by **hydrogen bonds**". This review focuses on supramolecular electron transfer pathways that can emerge on interlinking by **hydrogen bonds** and metal coordination of some unnoticed structures with pi-clouds in proteins and **nucleic acids**, potentially useful in catalysis and energy missions.

9/3,AB/2 (Item 2 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

09773558 99119199

Dual recognition of double-stranded DNA by 2'-aminoethoxy-**modified** oligonucleotides: the solution structure of an **intramolecular** triplex obtained by NMR spectroscopy.

Blommers MJ; Natt F; Jahnke W; Cuenoud B
Core Technologies, Novartis Pharma AG, Basel, Switzerland.

Biochemistry (UNITED STATES) Dec 22 1998, 37 (51) p17714-25, ISSN 0006-2960 Journal Code: A0G
Languages: ENGLISH
Document type: JOURNAL ARTICLE

The solution structure of an **intramolecular** triple helical oligonucleotide has been solved by NMR. The third strand of the pyrimidine x purine x pyrimidine triplex is composed of 2'-aminoethoxy-**modified** riboses, whereas the remaining part of the **nucleic acid** is DNA. The structure around the aminoethoxy **modification** was obtained with the help of selective isotope labeling in conjunction with isotope-editing experiments. Dinucleotide steps and interstrand connectivities, as well as the complete backbone conformation of the triplex, were derived from J-couplings, NOEs, and 31P chemical shifts. The structure of this triplex, solved by distance geometry, explains the extraordinary stability and increase in rate of triplex formation induced by 2'-aminoethoxy-**modified** oligonucleotides: apart from the formation of seven **base** triples, a well-defined **hydrogen-bonding** network is formed across the Crick-Hoogsteen groove involving the amino protons of the aminoethoxy moieties and the phosphates of the purine strand of the DNA. The **modified** strand adopts a conformation which is close to an A-type helix, whereas the DNA duplex conformation is best described as an unwound B-type helix. The groove dimensions and helical parameters of the 2'-aminoethoxy-**modified** rY x dRdY triplex are surprisingly well conserved in comparison with DNA triplexes.

9/3,AB/3 (Item 3 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

08239278 95127702

Solution conformation of the (-)-trans-anti-benzo[c]phenanthrene-dA ([BPh]dA) adduct opposite dT in a DNA duplex: intercalation of the covalently attached benzo[c]phenanthrenyl ring to the 3'-side of the adduct site and comparison with the (+)-trans-anti-[BPh]dA opposite dT stereoisomer.

Cosman M; La[redacted]ea A; Fiala R; Hingerty BE; Ami[redacted]S; Geacintov NE; Broyde S; Patel DJ

Cellular Biochemistry and Biophysics Program, Memorial Sloan-Kettering Cancer Center, New York, New York 10021.

Biochemistry (UNITED STATES) Jan 31 1995, 34 (4) p1295-307, ISSN 0006-2960 Journal Code: A0G

Contract/Grant No.: CA-46533, CA, NCI; CA-20851, CA, NCI; CA-28038, CA, NCI; +

Languages: ENGLISH

Document type: JOURNAL ARTICLE

This paper reports on NMR-molecular mechanics structural studies of the (-)- trans-anti-benzo[c]phenanthrene-dA adduct positioned opposite dT in the sequence context of the d(C1-T2-C3-T4-C5-[BPh]A6-C7-T8-T9-C10-C11).d(G12- G13-A14-A15-G16-T17-G18-A19-G20-A21- G22) duplex (designated as the (-)-trans-anti-[BPh]dA.dT 11-mer duplex). This adduct is derived from the covalent binding of (-)-1,2-dihydroxy-3,4-epoxy-1,2,3,4-tetrahydro-benzo[c] phenanthrene [(-)-anti-BPhDE] to N6 of dA6 in this duplex sequence. The benzo[c]phenanthrenyl and **nucleic acid** exchangeable and nonexchangeable protons were assigned in the predominant conformation following analysis of two-dimensional NMR data sets in H2O and D2O buffer solution. The solution structure of the (-)-trans-anti-[BPh]dA.dT 11-mer duplex has been determined by incorporating **intramolecular** and carcinogen-DNA proton-proton distances defined by lower and upper bounds deduced from NOESY data sets as restraints in molecular mechanics computations in torsion angle space. The results show that the [BPh]dA6.dT17 **base** pair propeller twists and buckles slightly to permit the covalently attached benzo[c]phenanthrenyl ring to intercalate between the [BPh]dA6.dT17 and dC7.dG16 **base** pairs to the 3'-side of the [BPh]dA6 lesion site without disrupting the Watson-Crick **hydrogen bond** alignments in the **modified** duplex. The strain in the highly sterically hindered fjord region of the benzo[c]phenanthrenyl moiety is relieved by the propeller-like nonplanar geometry of the aromatic phenanthrenyl ring system, which stacks predominantly with the dG16 and dT17 **bases** on the unmodified strand. The benzylic ring adopts a distorted half-chair form, in which the H1 and H2 protons are pseudo-diequatorial and the H3 and H4 protons are pseudodiaxial. The current observation that the (-)-trans-anti-[BPh]dA positioned opposite dT intercalates to the 3'-side of the intact **modified base** pair contrasts with our previous demonstration that the stereoisomeric (+)-trans-anti-[BPh]dA adduct positioned opposite dT intercalates to the 5'-side of the intact **modified base** pair [Cosman, M., et al. (1993b) Biochemistry 32, 12488-12497]. These stereochemically induced structural differences between isomeric [BPh]dA lesions derived from the binding of chiral (+)- and (-)-anti-BPhDE enantiomers may in turn profoundly influence the interactions of the carcinogen-**modified** DNA with repair and replication enzymes in the cell.

9/3,AB/4 (Item 4 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

07626029 93181161

Protonated pyrimidine-purine-purine triplex.

Malkov VA; Voloshin ON; Veselkov AG; Rostapshov VM; Jansen I; Soyfer VN; Frank-Kamenetskii MD

Institute of Molecular Genetics, Russian Academy of Science, Moscow.

Nucleic acids research (ENGLAND) Jan 11 1993, 21 (1) p105-11, ISSN 0305-1048 Journal Code: O8L

Contract/Grant No.: GM44700-02, GM, NIGMS

Languages: ENGLISH

Document type: JOURNAL ARTICLE

We have studied a protonated pyrimidine-purine-purine (Py-Pu-Pu) triplex, which is formed between the d(C)nd(G)n duplex and the d(AG)m oligonucleotide as the third strand and carries the CG*A+ protonated

base -triads. We have observed such an intermolecular complex between a plasmid carrying the d(C)18 d(G)18 insert and the d(AG)5 oligonucleotide without bivalent cations in 200 mM of Na+ at pH4.0. Bivalent cations additionally stabilize the complex. We propose the structures for nearly isomorphous **base** -triads TA*A, CG*G and CG*A+. To identify the H-DNA-like structure, which includes the triplex between d(C)n d(G)n duplex and the AG-strand, we have cloned in a superhelical plasmid the insert: G10TTAA(AG)5. The data on photofootprinting and chemical **modification** with diethyl pyrocarbonate, potassium permanganate and dimethyl sulfate demonstrate that the H-like structure with triplex carrying CG*G and CG*A+ **base** triads is actually formed under acid conditions. In the course of this study we have come across unexpected results on probing of Py-Pu-Pu triplexes by dimethyl sulfate (DMS): the protection effect is observed not only for guanines entering the duplex but also for guanines in the third strand lying in the major groove. We have demonstrated this effect not only for the case the novel protonated Py-Pu-Pu triplex but also for the traditional non-protonated Py-Pu-Pu **intramolecular** triplex (H*-DNA) formed by the d(C)37 d(G)37 insert in supercoiled plasmid in the presence of Mg2+ ions.

9/3,AB/5 (Item 5 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07533937 93237220

Solution conformation of the (+)-cis-anti-[BP]dG adduct in a DNA duplex: intercalation of the covalently attached benzo[a]pyrenyl ring into the helix and displacement of the **modified** deoxyguanosine.

Cosman M; de los Santos C; Fiala R; Hingerty BE; Ibanez V; Luna E; Harvey R; Geacintov NE; Broyde S; Patel DJ

Department of Biochemistry and Molecular Biophysics, College of Physicians and Surgeons, Columbia University, New York, New York 10032.

Biochemistry (UNITED STATES) Apr 27 1993, 32 (16) p4145-55, ISSN 0006-2960 Journal Code: A0G

Contract/Grant No.: CA-46533, CA, NCI; CA-21111, CA, NCI; CA-09503, CA, NCI; +

Languages: ENGLISH

Document type: JOURNAL ARTICLE

This paper reports on the solution structure of the (+)-cis-anti-[BP]dG adduct positioned opposite dC in a DNA oligomer duplex which provides the first experimentally **based** solution structure of an intercalative complex of a polycyclic aromatic hydrocarbon covalently bound to the N2 of deoxyguanosine. The combined NMR-energy minimization computation studies were undertaken on the (+)-cis-anti-[BP]dG adduct embedded in the same d(C5-[BP]G6-C7).d(G16-C17-G18) trinucleotide segment of the complementary 11-mer duplex studied previously with the stereoisomeric trans adducts. The exchangeable and nonexchangeable protons of the benzo[a]pyrenyl moiety and the **nucleic acid** were assigned following analysis of two-dimensional NMR data sets in H2O and D2O solution. The solution structure of the (+)-cis-anti-[BP]dG-dC 11-mer duplex has been determined by incorporating **intramolecular** and intermolecular proton-proton distances defined by upper and lower bounds deduced from NOESY data sets as restraints in energy minimization computations. The benzo[a]pyrene ring of [BP]dG6 is intercalated between intact Watson-Crick dC5.dG18 and dC7.dG16 **base** pairs in a right-handed DNA helix. The benzylic ring is in the minor groove while the pyrenyl ring stacks with flanking dC5 and dC7 **bases** on the same strand. The deoxyguanosine ring of [BP]dG6 is not Watson-Crick **base** paired but displaced into the minor groove with its plane parallel to the helix axis and stacks over the sugar ring of dC5. The dC17 **base** on the partner strand is displaced from the center of the helix toward the major groove by the intercalated benzo[a]pyrene ring. This intercalative structure of the (+)-cis-anti-[BP]dG-dC 11-mer duplex exhibits several unusually shifted proton resonances which can be readily accounted for by the ring current contributions of the deoxyguanosine and

pyrenyl rings of the [BP]dG6 adduct. Several phosphorus resonances are shifted to low and high field of the unperturbed phosphorus spectral region and have been assigned to internucleotide phosphates centered about the [BP]dG6 **modification** site. These studies define the changes in the helix at the central trinucleotide segment needed to generate the intercalation site for the covalently bound (+)-cis-anti-[BP]dG adduct.(ABSTRACT TRUNCATED AT 400 WORDS)

9/3,AB/6 (Item 6 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07418839 91307670
Conformational preferences of **modified nucleic acid bases** N6-methyl-N6-(N-threonylcarbonyl) adenine and 2-methylthio-N6-(N-threonylcarbonyl) adenine by the quantum chemical PCILO calculations.
Tewari R
Physical Chemistry Division, National Chemical Laboratory, Pune, India.
Journal of biomolecular structure & dynamics (UNITED STATES) Dec 1990, 8 (3) p675-86, ISSN 0739-1102 Journal Code: AH2
Languages: ENGLISH
Document type: JOURNAL ARTICLE
Conformational preferences of the hypermodified **nucleic acid bases** N6-methyl-N6-(N-threonylcarbonyl) Adenine, m6tc6 Ade, and 2-methylthio-N6-(N-threonylcarbonyl) Adenine, mS2 tc6 Ade, have been studied theoretically using the quantum chemical PCILO (Perturbative Configuration Interaction using Localized Orbitals) method. The multidimensional conformational space has been searched using selected grid points formed by combining the various torsion angles which take the favoured values obtained from energy variation with respect to each torsion angle individually. In m6 tc6 Ade and mS 2tc6 Ade alike the threonylcarbonyl substituent preferably orients away (distal) from the imidazole moiety of the adenine ring. And as in the simpler N6-(N-threonylcarbonyl) Adenine, tc6 Ade, the atoms in the ureido group as well as the amino acid carbon atoms C(12) and C(13) remain coplanar with the purine **base** . As in tc6 Ade, this conformation is stabilized by the **intramolecular hydrogen bond** between N(11)H of the amino acid and N(1) of the adenine **base**. The N6-methyl protons, in m6 tc6 Ade, take trans-staggered orientation with respect to the C(6)-N(6) bond. The preferred orientation of the 2-methylthio group is cis to the C(2)-N(3) bond in mS 2tc6 Ade. This is in marked contrast to the **modified nucleic acid base** 2-methylthio-N6-(delta 2-isopentenyl) Adenine, mS 2i6 Ade, where the 2-methylthio group orients trans to the C(2)-N(3) bond, causing a change in the preferred orientation of the isopentenyl component on methylthiolation. The present results thus indicate that unlike in the isopentenyl adenine the role of further chemical substitutions in threonylcarbonyl adenine may be indirect and less pronounced.

9/3,AB/7 (Item 7 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07323027 92297634
Influence of benzo[a]pyrene diol epoxide chirality on solution conformations of DNA covalent adducts: the (-)-trans-anti-[BP]G.C adduct structure and comparison with the (+)-trans-anti-[BP]G.C enantiomer.
de los Santos C; Cosman M; Hingerty BE; Ibanez V; Margulis LA; Geacintov NE; Broyde S; Patel DJ
Department of Biochemistry and Molecular Biophysics, College of Physicians and Surgeons, Columbia University, New York, New York 10032.
Biochemistry (UNITED STATES) Jun 16 1992, 31 (23) p5245-52, ISSN 0006-2960 Journal Code: A0G

Contract/Grant No.: CA-2111, CA, NCI; CA-09503, CA, NCI; CA-20851, CA, NCI; +
Languages: ENGLISH
Document type: JOURNAL ARTICLE

Benzo[a]pyrene (BP) is an environmental genotoxin, which, following metabolic activation to 7,8-diol 9,10-epoxide (BPDE) derivatives, forms covalent adducts with cellular DNA. A major fraction of adducts are derived from the binding of N2 of guanine to the C10 position of BPDE. The mutagenic and carcinogenic potentials of these adducts are strongly dependent on the chirality at the four asymmetric benzylic carbon atoms. We report below on the combined NMR-energy minimization refinement characterization of the solution conformation of (-)-trans-anti-[BP]G positioned opposite C and flanked by G.C **base** pairs in the d(C1-C2-A3-T4-C5-[BP]G6-C7-T8-A9-C10-C11).d(G12-G13-T14++ +-A15-G16-C17-G18-A19-T20-G21-G22) duplex. Two-dimensional NMR techniques were applied to assign the exchangeable and non-exchangeable protons of the benzo[a]pyrenyl moiety and the **nucleic acid** in the **modified** duplex. These results establish Watson-Crick **base** pair alignment at the [BP]G6.C17 **modification** site, as well as the flanking C5.G18 and C7.G16 pairs within a regular right-handed helix. The solution structure of the (-)-trans-anti-[BP]G.C 11-mer duplex has been determined by incorporating **intramolecular** and intermolecular proton-proton distances defined by lower and upper bounds deduced from NOE buildup curves as constraints in energy minimization computations. The BP ring spans both strands of the duplex in the minor groove and is directed toward the 3'-end of the **modified** strand in the refined structure. One face of the BP ring of [BP]G6 stacks over the C17 residue across from it on the partner strand while the other face is exposed to solvent.(ABSTRACT TRUNCATED AT 250 WORDS)

9/3,AB/8 (Item 8 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07249159 93041779
Solution structure of the covalent sterigmatocystin-DNA adduct.
Gopalakrishnan S; Liu X; Patel DJ
Department of Biochemistry and Molecular Biophysics, College of Physicians and Surgeons, Columbia University, New York, New York 10032.
Biochemistry (UNITED STATES) Nov 10 1992, 31 (44) p10790-801, ISSN 0006-2960 Journal Code: A0G
Contract/Grant No.: CA46533, CA, NCI
Languages: ENGLISH
Document type: JOURNAL ARTICLE

Sterigmatocystin and aflatoxin are potent mutagens that contaminate foodstuffs stored under conditions that permit fungal growth. These food mycotoxins can be metabolically activated to their epoxides, which subsequently form covalent adducts with DNA and can eventually induce tumor development. We have generated the sterigmatocystin-d(A1-A2-T3-G4-C5-A6-T7-T8) covalent adduct (two sterigmatocystins per duplex) by reacting sterigmatocystin-1,2-epoxide with the self-complementary d(A-A-T-G-C-A-T-T) duplex and determined its solution structure by the combined application of two-dimensional NMR experiments and molecular dynamics calculations. The self-complementary duplex retains its 2-fold symmetry following covalent adduct formation of sterigmatocystin at the N7 position of G4 residues on each strand of the duplex. The H8 proton of [ST]G4 exchanges rapidly with water and resonates at 9.58 ppm due to the presence of the positive charge on the guanine ring following adduct formation. We have assigned the exchangeable and nonexchangeable proton resonances of sterigmatocystin and the duplex in the covalent adduct and identified the intermolecular proton-proton NOEs that define the orientation and mode of binding of the mutagen to duplex DNA. The analysis was aided by intermolecular NOEs between the sterigmatocystin protons with both the major groove and minor groove protons of the DNA. The molecular dynamics calculations were aided

by 180 **intramolecular nucleic acid** constraints, 16 **intramolecular** sterigmatocystin constraints, and 56 intermolecular distance constraints between sterigmatocystin and the **nucleic acid** protons in the adduct. The sterigmatocystin chromophore intercalates between the [ST]G4.C5 and T3.A6 **base** pairs and stacks predominantly over the **modified** guanine ring in the adduct duplex. The overall conformation of the DNA remains right-handed on adduct formation with unwinding of the helix, as well as widening of the minor groove. Parallel NMR studies on the sterigmatocystin-d(A1-A2-A3-G4-C5-T6-T7-T8) covalent adduct (two sterigmatocystins per duplex) provide supportive evidence that the mutagen covalently adducts the N7 position of G4 and its chromophore intercalates to the 5' side of the guanine and stacks over it. The present NMR-molecular dynamics studies that define a detailed structure for the sterigmatocystin-DNA adduct support key structural conclusions proposed previously on the basis of a qualitative analysis of NMR parameters for the adduct formed by the related food mutagen aflatoxin B1 and DNA [Gopalakrishnan, S., Harris, T. M., & Stone, M. P. (1990) Biochemistry 29, 10438-10448].

9/3,AB/9 (Item 9 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07182031 93091145
Conformational perturbation of the anticancer nucleotide arabinosylcytosine on Z-DNA: molecular structure of (araC-dG)3 at 1.3 A resolution.
Zhang H; van der Marel GA; van Boom JH; Wang AH
Division of Biophysics, University of Illinois, Champaign, Urbana 61801.
Biopolymers (UNITED STATES) Nov 1992, 32 (11) p1559-69, ISSN 0006-3525 Journal Code: A5Z
Contract/Grant No.: GM-41612, GM, NIGMS; CA-52506, CA, NCI
Languages: ENGLISH
Document type: JOURNAL ARTICLE
The left-handed Z-DNA structure of an araC-containing (where araC stands for arabinosylcytosine) hexamer, (araC-dG)3, has been solved by x-ray diffraction analysis at 1.3 A resolution. This hexamer was crystallized in the hexagonal P6(5)22 (a = b = 17.96 A, c = 43.22 A) space group in which the hexamers have statistically disordered packing arrangement along the 6(5) screw axis, yet the crystals diffract x-rays to high resolution. Its structure has been refined by the constrained least square refinement to a final R factor of 0.287 using 737 [> 3.0 sigma(F)] observed reflections. The asymmetric unit of the unit cell contains only a dinucleotide, 5'-p(araC)p(dG). The overall conformation resembles that of the canonical Z-DNA, but with some differences in details. The O2' hydroxyl groups of the araC residues form **intramolecular hydrogen bonds** with N2 of the 5'-guanine residues. In the deep groove of Z-DNA, these hydroxy groups replace the bridging water molecules that stabilize the guanine in the syn conformation. The results reinforce the earlier observation made by the structural analysis of another hexamer, d(CG[araC]GCG), with a mono-substitution of araC [M.-K. Teng, Y.-C. Liaw, G. A. van der Marel, J. H. van Boom, and A. H.-J. Wang (1989). Biochemistry, vol. 28, pp. 4923-4928]. These two structures show that araC residue can be incorporated readily into the Z structure and probably facilitates the B to Z transition, as supported by uv absorption spectroscopic studies in a number of araC-containing oligonucleotides. The potential biological roles of the araC-**modified** Z-DNA are discussed.

9/3,AB/10 (Item 10 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

06782384 92002042

Molecular structure of a DNA decamber containing an anticancer nucleoside arabinosylcytosine: conformational perturbation by arabinosylcytosine in B-DNA.

Gao YG; van der Marel GA; van Boom JH; Wang AH
Department of Physiology and Biophysics, University of Illinois, Urbana-Champaign 61801.

Biochemistry (UNITED STATES) Oct 15 1991, 30 (41) p9922-31, ISSN 0006-2960 Journal Code: A0G
Contract/Grant No.: GM-41612, GM, NIGMS; CA-52506, CA, NCI
Languages: ENGLISH
Document type: JOURNAL ARTICLE

Arabinosylcytosine (araC) is an important anticancer drug that has been shown to be misincorporated into DNA double helix. The incorporation of araC into DNA may have significant conformational consequences that could affect the function of DNA. In this paper, we present the high-resolution 3D structure of an araC-containing decamer d[CCAGGC(araC)TGG], as determined by X-ray diffraction analysis, and assess the possible DNA structural perturbation induced by araC. The **modified** decamer was crystallized in the monoclinic C2 (a = 31.97 A, b = 25.56 A, c = 34.62 A and beta = 114.50 degrees) space group, the same as that from d(CCAGGCCTGG) [Heinemann, U., & Alings, C. (1989) J. Mol. Biol. 210, 369]. The structure of the araC-containing decamer was solved by the molecular replacement method and refined by the constrained least-squares refinement procedure to obtain a final R factor of 0.187 using 2349 [greater than 2.0 sigma(F)] observed reflections to a resolution of 1.6 A. The overall conformation resembles that of the canonical decamer DNA structure, but with significant differences in regions close to the araC site. The O2' hydroxyl groups of the araC residues lie in the major groove of the helix, and they are in close contact with the C5 methyl and C6 H6 atoms of the thymine on the 3'-side. This creates a higher buckle in the araC7-G14 **base** pair (14 degrees), as compared to that found in the canonical decamer (9 degrees). This may slightly destabilize B-DNA. No direct **intramolecular hydrogen bond** is formed, in contrast to the situation when araC is incorporated into Z-DNA.(ABSTRACT TRUNCATED AT 250 WORDS)

9/3,AB/11 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

05759527 BIOSIS NO.: 000084107934
THEORETICAL STUDIES ON CONFORMATIONAL PREFERENCES OF **MODIFIED NUCLEIC ACID BASE** N-6-N THREONYLCARBONYL ADENINE

AUTHOR: TEWARI R
AUTHOR ADDRESS: PHYSICAL CHEM. DIV., NATL. CHEM. LAB., PUNE 411 008.

JOURNAL: INDIAN J BIOCHEM BIOPHYS 24 (3). 1987. 170-176.
FULL JOURNAL NAME: Indian Journal of Biochemistry and Biophysics
CODEN: IJBBB
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: Conformational preferences of **modified nucleic acid base** N6-(N-threonylcarbonyl)adenine, tc6Ade, have been investigated using the quantum chemical PCILO method. The multidimensional conformational space has been searched using selected grid points formed by combining the various torsion angles which take the favoured values obtained from energy variation with respect to each torsion angle individually. The predicted most stable conformation of the molecule is such that the substituent is oriented away (distal) from the imidazole moiety of the adenine ring. The atoms in the ureido group as well as the amino acid carbon atoms C(12) and C(13) remain coplanar with the purine **base**. The **intramolecular hydrogen bond** involving N(11)H of the amino acid and N(1) of the adenine **base** provides the principal contribution to the molecular stabilisation. The indicated flexible orientations for the carboxyl group and the threonine

residue may enable probing of the molecular environment, in the vicinity of the anti[illegible]on in tRNA, by the amino acid [illegible]stituent without excessive energy destabilisation.
? t s11/3,ab/all

11/3,AB/1 (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

10230908 20073016
Assignment of cytosine N3 resonances in **nucleic acids** via intrabase three-bond coupling to amino protons.
Rudisser S; Pelton JG; Tinoco I Jr
Department of Chemistry, University of California, Berkeley, USA.
Journal of biomolecular NMR (NETHERLANDS) Oct 1999, 15 (2) p173-6, ISSN 0925-2738 Journal Code: BJM
Contract/Grant No.: GM 10840, GM, NIGMS
Languages: ENGLISH
Document type: JOURNAL ARTICLE
Coherences were observed between 15N3 of cytosine and its trans amino proton (H42) using a **modified** gradient-**based** heteronuclear single quantum coherence (HSQC) pulse sequence optimized for three-bond proton-nitrogen couplings. The method is demonstrated with a 22-nucleotide RNA fragment of the P5abc region of a group I intron uniformly labeled with 15N. Use of intraresidue 15N3-amino proton couplings to assign cytosine 15N3 signals **complements** the recently proposed JNN HNN COSY [Dingley, A.J. and Grzesiek, S. (1998) J. Am. Chem. Soc., 120, 8293-8297] method of identifying **hydrogen-bonded base** pairs in RNA.

11/3,AB/2 (Item 2 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

10026801 99379831
Solution structures of aminofluorene [AF]-stacked conformers of the syn [AF]-C8-dG adduct positioned opposite dC or dA at a template-primer junction.
Gu Z; Gorin A; Hingerty BE; Broyde S; Patel DJ
Cellular Biochemistry and Biophysics Program, Memorial Sloan-Kettering Cancer Center, New York 10021, USA.
Biochemistry (UNITED STATES) Aug 17 1999, 38 (33) p10855-70, ISSN 0006-2960 Journal Code: A0G
Contract/Grant No.: CA-49982, CA, NCI; CA-75449, CA, NCI; CA-28038, CA, NCI; +
Languages: ENGLISH
Document type: JOURNAL ARTICLE
A solution structural study has been undertaken on the aminofluorene-C8-dG ([AF]dG) adduct located at a single-strand-double-stran d d(A1-A2-C3-[AF]G4-C5-T6-A7-C8-C9-A10-T11-C12-C13).d(G14-G15-A16-T17-G18-G19-T20- A21-G22-N23) 13/10-mer junction (N = C or A) using proton-proton distance restraints derived from NMR data in combination with intensity-**based** relaxation matrix refinement computations. This single-strand-double-strand junction models one arm of a replication fork composed of a 13-mer template strand which contains the [AF]dG **modification** site and a 10-mer primer strand which has been elongated up to the **modified** guanine with either its **complementary** dC partner or a dA mismatch. The solution structures establish that the duplex segment retains a minimally perturbed B-DNA conformation with Watson-Crick **hydrogen-bonding** retained up to the dC5.dG22 **base** pair. The guanine ring of the [AF]dG4 adduct adopts a syn glycosidic torsion angle and is displaced into the major groove when positioned opposite dC or dA residues. This **base** displacement of the **modified** guanine is accompanied by stacking of one face of the aminofluorene ring of [AF]dG4

with the dG5.dG22 **base** pair, while the other face of the aminofluorene ring is stacked with the purine ring of the nonadjacent dA2 residue. By contrast, the dC and dA residues opposite the junctional [AF]dG4 adduct site adopt distinctly different alignments. The dC23 residue positioned opposite the adduct site is looped out into the minor groove by the aminofluorene ring. The syn displaced orientation of the **modified** dG with stacking of the aminofluorene and the looped out position of the partner dC could be envisioned to cause polymerase stalling associated with subsequent misalignment leading to frameshift mutations in appropriate sequences. The dA23 residue positioned opposite the adduct site is positioned in the major groove with its purine ring aligned face down over the van der Waals surface of the major groove and its amino group directed toward the T6.A21 **base** pair. The Hoogsteen edge of the **modified** guanine of [AF]dG4 and the Watson-Crick edge of dA23 positioned opposite it are approximately coplanar and directed toward each other but are separated by twice the **hydrogen-bonding** distance required for pairing. This structure of [AF]dG opposite dA at a model template-primer junctional site can be compared with a previous structure of [AF]dG opposite dA within a fully paired duplex [Norman, D., Abuaf, P., Hingerty, B. E., Live, D., Grunberger, D., Broyde, S., and Patel, D. J. (1989) Biochemistry 28, 7462-7476]. The alignment of the Hoogsteen edge of [AF]dG (syn) positioned opposite the Watson-Crick edge of dA (anti) has been observed for both systems with the separation greater in the case of the junctional alignment in the model template-primer system. However, the aminofluorene ring is positioned in the minor groove in the fully paired duplex while it stacks over the junctional **base** pair in the template-primer system. This suggests that the syn [AF]dG opposite dA junctional alignment can be readily incorporated within a duplex by a translation of this entity toward the minor groove.

11/3,AB/3 (Item 3 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

09988777 99269784

High-performance subtractive hybridization of cDNAs by covalent bonding between specific **complementary** nucleotides

Ying SY; Lin S

Department of Cell and Neurobiology, University of Southern California School of Medicine, Los Angeles 90033, USA.

BioTechniques (UNITED STATES) May 1999, 26 (5) p966-8, 970-2, 979 passim, ISSN 0736-6205 Journal Code: AN3.

Languages: ENGLISH

Document type: JOURNAL ARTICLE

We have developed an improved subtractive hybridization method that provides a fast, simple and reliable isolation of desired different sequences from two compared DNA libraries, one of which contains all unwanted homologues (subtracter) and another contains certain desired heterologues (tester). The DNA library can be made from either mRNA or genomic DNA. An excess amount of **modified** subtracter DNA from control cells was generated by chemical carboxylation of the pyrimidines to provide covalent affinity to the purines of a natural tester DNA. Hybridization of the control subtracter and the experimental tester DNA was performed with a heat-melting and then cool-reassociation technique. The desired different sequences remained in the form of **hydrogen-bonded**, homologous sequences of both libraries covalently bonded to each other, resulting in no separation during PCR and cloning. Consequently, the DNA sequences obtained from the covalent homology subtraction represent the nucleotide sequences abundant in the tester but rare in the subtracter library.

11/3,AB/4 (Item 4 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

09950395 99[redacted]819
Discrimination of DNA hybridization using chemical force microscopy.
Mazzola LT; Frank CW; Fodor SP; Mosher C; Lartius R; Henderson E
Department of Chemistry, Stanford University, Stanford, California 94305, USA.
Biophysical journal (UNITED STATES) Jun 1999, 76 (6) p2922-33, ISSN 0006-3495 Journal Code: A5S
Languages: ENGLISH
Document type: JOURNAL ARTICLE

Atomic force microscopy (AFM) can be used to probe the mechanics of molecular recognition between surfaces. In the application known as "chemical force" microscopy (CFM), a chemically **modified** AFM tip probes a surface through chemical recognition. When **modified** with a biological ligand or receptor, the AFM tip can discriminate between its biological binding partner and other molecules on a heterogeneous substrate. The strength of the interaction between the **modified** tip and the substrate is governed by the molecular affinity. We have used CFM to probe the interactions between short, segments of single-strand DNA (oligonucleotides). First, a latex microparticle was **modified** with the sequence 3'-CAGTTCTACGATGGCAAGTC and epoxied to a standard AFM cantilever. This DNA-**modified** probe was then used to scan substrates containing the **complementary** sequence 5'-GTCAAGATGCTACCGTTCAG. These substrates consisted of micron-scale, patterned arrays of one or more distinct oligonucleotides. A strong friction interaction was measured between the **modified** tip and both elements of surface-bound DNA. **Complementary** oligonucleotides exhibited a stronger friction than the noncomplementary sequences within the patterned array. The friction force correlated with the measured strength of adhesion (rupture force) for the tip- and array-bound oligonucleotides. This result is consistent with the formation of a greater number of **hydrogen bonds** for the **complementary** sequence, suggesting that the friction arises from a sequence-specific interaction (hybridization) of the tip and surface DNA.

11/3,AB/5 (Item 5 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

09931348 99272652
Recognition of nonhybridizing **base** pairs during nucleotide excision repair of DNA.
Buschta-Hedayat N; Buterin T; Hess MT; Missura M; Naegeli H
Institute of Pharmacology and Toxicology, University of Zurich-Tierspital, August Forel-Strasse 1, 8008 Zurich, Switzerland.
Proceedings of the National Academy of Sciences of the United States of America (UNITED STATES) May 25 1999, 96 (11) p6090-5, ISSN 0027-8424 Journal Code: PV3
Languages: ENGLISH
Document type: JOURNAL ARTICLE

Nondistorting C4' backbone adducts serve as molecular tools to analyze the strategy by which a limited number of human nucleotide excision repair (NER) factors recognize an infinite variety of DNA lesions. We have constructed composite DNA substrates containing a noncomplementary site adjacent to a nondistorting C4' adduct to show that the loss of **hydrogen bonding** contacts between partner strands is an essential signal for the recruitment of NER enzymes. This specific conformational requirement for excision is mediated by the affinity of xeroderma pigmentosum group A (XPA) protein for nonhybridizing sites in duplex DNA. XPA recognizes defective Watson-Crick **base** pair conformations even in the absence of DNA adducts or other covalent **modifications**, apparently through detection of hydrophobic **base** components that are abnormally exposed to the double helical surface. This recognition function of XPA is enhanced by replication protein A (RPA) such that, in combination, XPA and RPA constitute a potent molecular sensor of

denatured **base** pairs. Our results indicate that the XPA-RPA complex may promote damage recognition by monitoring Watson-Crick **base** pair integrity, thereby recruiting the human NER system preferentially to sites where hybridization between **complementary** strands is weakened or entirely disrupted.

11/3,AB/6 (Item 6 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

09705692 99029892
Structure-function relationships in the hammerhead ribozyme probed by **base** rescue.
Peracchi A; Matulic-Adamic J; Wang S; Beigelman L; Herschlag D
Department of Biochemistry, Stanford University, California 94305-5307, USA.
RNA (UNITED STATES) Nov 1998, 4 (11) p1332-46, ISSN 1355-8382
Journal Code: CHB
Contract/Grant No.: GM49243, GM, NIGMS
Languages: ENGLISH
Document type: JOURNAL ARTICLE
We previously showed that the deleterious effects from introducing abasic nucleotides in the hammerhead ribozyme core can, in some instances, be relieved by exogenous addition of the ablated **base** and that the relative ability of different **bases** to rescue catalysis can be used to probe functional aspects of the ribozyme structure [Peracchi et al., Proc NatAcad Sci USA 93:11522]. Here we examine rescue at four additional positions, 3, 9, 12 and 13, to probe transition state interactions and to demonstrate the strengths and weaknesses of **base** rescue as a tool for structure-function studies. The results confirm functional roles for groups previously probed by mutagenesis, provide evidence that specific interactions observed in the ground-state X-ray structure are maintained in the transition state, and suggest formation in the transition state of other interactions that are absent in the ground state. In addition, the results suggest transition state roles for some groups that did not emerge as important in previous mutagenesis studies, presumably because **base** rescue has the ability to reveal interactions that are obscured by local structural redundancy in traditional mutagenesis. The **base** rescue results are **complemented** by comparing the effects of the abasic and phenyl nucleotide substitutions. The results together suggest that stacking of the **bases** at positions 9, 13 and 14 observed in the ground state is important for orienting other groups in the transition state. These findings add to our understanding of structure-function relationships in the hammerhead ribozyme and help delineate positions that may undergo rearrangements in the active hammerhead structure relative to the ground-state structure. Finally, the particularly efficient rescue by 2-methyladenine at position 13 relative to adenine and other **bases** suggests that natural **base modifications** may, in some instance, provide additional stability by taking advantage of hydrophobic interactions in folded RNAs.

11/3,AB/7 (Item 7 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

09700458 99036631
Differential DNA recognition by the enantiomers of 1-Rh(MGP)2 phi: a combination of shape selection and direct readout.
Franklin SJ; Barton JK
Beckman Institute, Division of Chemistry and Chemical Engineering, California Institute of Technology, Pasadena 91125, USA.
Biochemistry (UNITED STATES) Nov 17 1998, 37 (46) p16093-105, ISSN 0006-2960 Journal Code: A0G

Contract/Grant No.: GM 33309, GM, NIGMS
Languages: ENGLISH
Document type: JOURNAL ARTICLE

The enantiomers of the symmetric metallointercalator complex 1-Rh(MGP)2phi5+ [MGP = 4-(guanidylmethyl)-1,10-phenanthroline; phi = phenanthrenequinone diimine] bound to DNA decamer duplexes containing their respective 6 bp recognition sequences have been investigated using 1H NMR. Shape selection due to the chirality of the metal center and **hydrogen -bonding** contacts of ancillary guanidinium groups to 3'-G N7 atoms define the recognition by complexes which bind by intercalation to duplex DNA. The titration of Lambda-Rh into the self-**complementary** decamer containing the recognition sequence (5'-GACATATGTC-3', L1) resulted in one symmetric bound conformation observed in the 1H NMR spectrum, indicating that the DNA duplex retains its symmetry in the presence of the metal complex. Upfield chemical shifts of duplex imino protons and the disruption of the NOE **base** -sugar contacts defined the central T5-A6 intercalation site. The downfield shift of the G8 imino proton supports the conclusion that the pendant guanidinium arms make simultaneous H-bonding contacts to the N7 atoms of 3'-G8 **bases** on either side of the site. A variable-temperature study of a partially titrated sample (2:3 Lambda-Rh/L1) showed the exchange rate (kobs) at 298 K to be 68 s-1 and the activation barrier to exchange (DeltaG of association) to be 2.7 kcal/mol, a value comparable to the stacking energy of one **base** step. The results presented coupled with biochemical data are therefore consistent with binding models in which Lambda-1-Rh(MGP)2phi5+ (Lambda-Rh) traps the recognition site 5'-CATATG-3' in an unwound state, permitting intercalation centrally and **hydrogen bonding** to guanines at the first and sixth **base** pair positions. The data suggest a different model of binding and recognition by Delta-Rh. The titration of Delta-Rh into a DNA decamer containing the 6 bp recognition site (D1, 5'-CGCATCTGAC-3'; D2, 5'-GTCAGATGCG-3') resulted in two, distinct conformers, in slow exchange on the NMR time scale. The rate of exchange between the two conformers (kobs) at 298 K is 37 s-1, most likely due to partial dissociation between binding modes. The slower rate relative to Lambda-Rh association reflects the relative rigidity of the D1 and/or D2 sequence in comparison to L1. NOE cross-peaks between the intercalating phi ligand and protons of T5-C6, as well as the upfield shifts observed for imino protons at this step, serve to define the central T5-C6 step as the single site of intercalation. The downfield shift of the 3'-G imino protons indicates the complex makes **hydrogen bond** contacts with these **bases**. The complex, which is too small to span a 6 bp B-form DNA sequence, nonetheless makes major groove contacts with 3'-G **bases** to either side of the site. Notably, both 3'-guanine **bases** are necessary to impart site specificity and slow dissociation kinetics with the 5'-CATCTG-3' site, as evidenced by the extremely exchange-broadened two-dimensional NOESY spectra of Delta-Rh bound to **modified** duplexes containing N7-deazaguanine at either G8 or G18; the loss of one major groove contact completely abolishes specificity for 5'-CATCTG-3'. DNA chemical shifts upon binding and intermolecular NOE contacts therefore support a model in which Delta-Rh intercalates in one of two canted binding conformations. Within this model, each intercalation mode allows one guanidinium-guanine **hydrogen bond** at a time, while bringing the other arm close to the phosphate backbone.

11/3,AB/8 (Item 8 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

09679879 98447628
Stereoselectivity of human nucleotide excision repair promoted by defective hybridization.
Hess MT; Naegeli H; Capobianco M
Institute of Pharmacology and Toxicology, University of Zurich-Tierspital, Winterthurerstrasse 260, CH-8057 Zurich, Switzerland.

Journal of [redacted]ological chemistry (UNITED STATES) Oct 23 1998, 273 (43) p27867-72, I[redacted] 0021-9258 Journal Code: HIV[redacted]
Languages: ENGLISH
Document type: JOURNAL ARTICLE

To assess helical parameters that dictate fast or slow removal of carcinogen-DNA adducts, we probed human nucleotide excision repair (NER) activity with DNA containing L-deoxyriboses. Unlike natural lesions such as pyrimidine dimers or **base** adducts, L-deoxyribonucleosides (the mirror images of normal D-deoxyribonucleosides) involve neither the addition nor the loss of covalent bonds or functional groups and hence exclude modulation of repair efficiency by adduct chemistry and size. Previous studies showed that single L-deoxyribonucleosides distort DNA backbones but are accommodated in the double helix with intact **hydrogen bonding** between **complementary** strands. Here, we found that such single L-enantiomers are rejected as excision repair substrates in a NER-proficient cell extract. However, the same L-deoxyribose moiety stimulates NER activity upon incorporation into a nonhybridizing site of one or, more effectively, two **base** mismatches. In contrast to single L-deoxyriboses, multiple consecutive L-deoxyriboses interfere with normal hybridization; in this case, the intrinsic derangement of **base** pairing was sufficient to promote the excision of a cluster of three adjacent L-deoxyribonucleosides without any requirement for mismatches. Thus, using stereoselective substrates, we demonstrate the participation of a recognition subunit that guides human NER activity to sites of defective Watson-Crick strand pairing. This conformational sensor detects labile **hydrogen bonds** irrespective of the type of deoxyribonucleotide **modification**.

11/3,AB/9 (Item 9 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

09452647 98190012

An intercalated and thermally stable FAPY adduct of aflatoxin B1 in a DNA duplex: structural refinement from 1H NMR.

Mao H; Deng Z; Wang F; Harris TM; Stone MP
Department of Chemistry and Center in Molecular Toxicology, Vanderbilt University, Nashville, Tennessee 37235, USA.

Biochemistry (UNITED STATES) Mar 31 1998, 37 (13) p4374-87, ISSN 0006-2960 Journal Code: A0G
Contract/Grant No.: CA-55678, CA, NCI; ES-03755, ES, NIEHS; RR-05805, RR, NCRR; +
Languages: ENGLISH
Document type: JOURNAL ARTICLE

The structure of a formamidopyrimidine (FAPY) adduct arising from imidazole ring opening of the initially formed trans-8, 9-dihydro-8-(N7-guanyl)-9-hydroxyaflatoxin B1 adduct under basic conditions and positioned in the 5'-d(CTATFAPYGATTCA)-3'*5'-d(TGAATCATAG)-3' oligodeoxynucleotide was determined. The FAPY adduct may be a major progenitor of aflatoxin B1-induced mutations in DNA. The freshly prepared sample showed biphasic melting, with transitions at 28 and 56 degreesC. NMR initially showed multiple subspectra. Over a period of several days at 4 degreesC, the sample converted to a single species with a Tm of 56 degreesC, 15 degrees C greater than the unmodified duplex. The deoxyribose was in the beta configuration about the anomeric carbon, evidenced by NOEs between FAPYG5 H3', H2', H2", and H1'. FAPY formation resulted in the loss of the guanine H8 proton, and the introduction of the formyl proton, which showed NOEs to FAPYG5 H1' and A6 N6Ha. A total of 31 NOEs from AFB1 to DNA protons were observed, mostly to the 5'-neighboring **base**, T4 in the **modified** strand. Sequential NOEs were interrupted between T4 and FAPYG5 in the **modified** strand, between C16 and A17 in the **complementary** strand, and between T4 N3H and FAPYG5 N1H. An NOE between FAPYG5 N1H and C16 N4H showed intact **hydrogen bonding** at FAPYG5*C16. Upfield chemical shifts were observed for T4 H6 and A17 H8.

Molecular dynamics calculations converged with pairwise rmsd differences of <0.9 A. The sixth root residual was 8.7 10(-2). The AFB1 moiety intercalated from the major groove between FAPYG5 and T4*A17, and stacked with T4 and FAPYG5 and partially stacked with A17. The **base** step between T4*A17 and FAPYG5*C16 was increased from 3.4 to 7 A. The duplex unwound by about 15 degrees. The FAPY formyl group was positioned to form a **hydrogen bond** with A6 N6Ha. Strong stacking involving the AFB1 moiety, and this **hydrogen bond** explains the thermal stabilization of four **base** pairs by this adduct, and may be a significant factor in its processing.

11/3,AB/10 (Item 10 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

09436190 98138692
The effect of pseudouridine and pH on the structure and dynamics of the anticodon stem-loop of tRNA(Lys,3).
Durant PC; Davis DR
Department of Medicinal Chemistry, University of Utah, Salt Lake City 84112, USA.
Nucleic acids symposium series (ENGLAND) 1997, (36) p56-7, ISSN 0261-3166 Journal Code: O8N
Contract/Grant No.: GM55508, GM, NIGMS; CA42014, CA, NCI; RR06262, RR, NCRR
Languages: ENGLISH
Document type: JOURNAL ARTICLE; REVIEW; REVIEW, TUTORIAL
The anticodon stem-loop hairpin of tRNA(Lys,3) was synthesized and the solution structure determined by NMR spectroscopy. The hairpin is thermodynamically stabilized by pseudouridine as determined by UV Tm measurements, and the local loop structure is stabilized with **base** -stacking of the nucleosides in the anticodon loop 5' of the psi 39 nucleoside **modification** . The tRNA(Lys,3) hairpin also contains an A(+)-C **base** -pair that effectively reduces the size of the normal 7 nucleotide anticodon loop to 5 nucleotides and induces a change in the loop backbone conformation. The stabilizing effects of the A(+)-C **base** -pair and pseudouridine are only partially additive, suggesting that the conformational changes caused by each **modification** are not completely compatible. The structure of the anticodon loop is distinctly different from that seen for other tRNAs exemplified by tRNA(Phe), suggesting that the full **complement** of **modified** nucleosides present in tRNA(Lys,3) should significantly change the structure compared to the unmodified tRNA anticodon loop. The conformation of the loop has important implications for the role of nucleoside **modification** in codon-anticodon recognition and for utilization of tRNA(Lys,3) by HIV-1 as the natural reverse transcriptase primer.

11/3,AB/11 (Item 11 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

09357280 97478543
Triplex formation at physiological pH: comparative studies on DNA triplexes containing 5-Me-dC tethered at N4 with spermine and tetraethyleneoxyamine.
Rajeev KG; Jadhav VR; Ganesh KN
Division of Organic Chemistry, National Chemical Laboratory, Pune 411008, India.
Nucleic acids research (ENGLAND) Nov 1 1997, 25 (21) p4187-93, ISSN 0305-1048 Journal Code: O8L
Languages: ENGLISH
Document type: JOURNAL ARTICLE
Oligodeoxynucleotides with spermine conjugation at C4 of 5-Me-dC (sp

-ODN) exhibit triple helix formation with **complementary** Watson-Crick duplexes, and were optimally stable at physiological pH 7.3 and low salt concentration. This was attributed to a favored reassociation of the polycationic third strand with the anionic DNA duplex. To gain further insights into the factors that contribute to the enhancement of triplex stability and for engineering improved triplex systems, the spermine appendage at C4 of 5-Me-dC was replaced with 1,11-diamino-3,6,9-trioxaundecane to create teg -ODNs. From the triple helix forming abilities of these **modified** ODNs studied by hysteresis behaviour and the effect of salts on triplex stability, it is demonstrated here that teg- ODNs stabilise triplexes through hydrophobic desolvation while sp -ODNs stabilise triplexes by charge effects. The results imply that factors in addition to **base** stacking effects and interstrand **hydrogen bonds** are significantly involved in modulation of triplex stability by **base modified** oligonucleotides.

11/3,AB/12 (Item 12 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

09144260 97299766

Solution structure of a DNA decamer containing the antiviral drug ganciclovir: combined use of NMR, restrained molecular dynamics, and full relaxation matrix refinement.

Foti M; Marshalko S; Schurter E; Kumar S; Beardsley GP; Schweitzer BI
Walt Disney Memorial Cancer Institute at Florida Hospital, Orlando 32826, USA.

Biochemistry (UNITED STATES) May 6 1997, 36 (18) p5336-45, ISSN 0006-2960 Journal Code: A0G
Languages: ENGLISH
Document type: JOURNAL ARTICLE

The nucleoside analog 9-[(1,3-dihydroxy-2-propoxy)methyl]guanine (ganciclovir, DHPG) is an antiviral drug that is used in the treatment of a variety of herpes viruses in immunocompromised patients and in a gene therapy protocol that has shown promising activity for the treatment of cancer. To probe the structural effects of ganciclovir when incorporated into DNA, we determined and compared the solution structure of a **modified** ganciclovir-containing decamer duplex [d(CTG)(ganciclovir)d(ATCCAG)]2 and a control duplex d[(CTGCATCCAG)]2 using nuclear magnetic resonance techniques. 1H and 31P resonances in both duplexes were assigned using a combination of 2-D 1H and 31P NMR experiments. Proton-proton distances determined from NOESY data and dihedral angles determined from DQF-COSY data were used in restrained molecular dynamics simulations starting from canonical A- and B-form DNA models. Both the control and ganciclovir sets of simulations converged to B-type structures. These structures were subjected to full relaxation matrix refinement to produce final structures that were in excellent agreement with the observed NOE intensities. Examination of the final ganciclovir-containing structures reveals that the **base** of the ganciclovir residue is **hydrogen bonded** to its **complementary** dC and is stacked in the helix; in fact, the **base** of ganciclovir exhibits increased stacking with the 5' **base** relative to the control. Interestingly, some of the most significant distortions in the structures occur 3' to the lesion site, including a noticeable kink in the sugar-phosphate backbone at this position. Further examination reveals that the backbone conformation, sugar pucker, and glycosidic torsion angle of the residue 3' to the lesion site all indicate an A-type conformation at this position. A possible correlation of these structural findings with results obtained from earlier biochemical studies will be discussed.

11/3,AB/13 (Item 13 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

09067257 97[redacted]14
Solution structure of the calicheamicin gamma 1I-DNA complex.
Kumar RA; Ikemoto N; Patel DJ
Cellular Biochemistry and Biophysics Program Memorial-Sloan Kettering Cancer Center, New York, NY 10021, USA.
Journal of molecular biology (ENGLAND) Jan 17 1997, 265 (2) p187-201, ISSN 0022-2836 Journal Code: J6V
Contract/Grant No.: CA 46778, CA, NCI
Languages: ENGLISH
Document type: JOURNAL ARTICLE

Calicheamicin gamma 1I is an enediyne antibiotic possessing antitumour activity associated with its ability to bind and following activation, affect double-strand cleavage at oligopyrimidine-oligopurine tracts on DNA. Footprinting and chemical **modification** studies have identified the (T-C-C-T).(A-G-G-A) sequence as a preferred calicheamicin gamma 1I binding site and established the importance of the 5'-guanine residue as critical for high affinity binding. The sequence specificity of intermolecular recognition has been identified with the aryltetrasaccharide component of the drug together with an important contribution from the iodine atom on the thiobenzoate ring to the affinity of complex formation. Calicheamicin gamma 1I binds to the minor groove of the DNA duplex and in the process positions the enediyne ring to abstract hydrogen atoms from partner strands leading to double-strand cleavage. We report on the solution structure of the calicheamicin gamma 1I-DNA hairpin duplex complex containing a central (T-C-C-T).(A-G-G-A) segment **based** on a combined analysis of NMR and molecular dynamics calculations including intensity refinement in a water box. The refined solution structures of the complex provide a molecular explanation of the sequence specificity of binding and cleavage by this member of the enediyne family of antitumor antibiotics. Calicheamicin gamma 1I binds to the DNA minor groove with its aryltetrasaccharide segment in an extended conformation spanning the (T-C-C-T).(A-G-G-A) segment of the duplex. Further, the thio sugar B molecule and the thiobenzoate ring C molecule are inserted in an edgewise manner deep into the minor groove with their faces sandwiched between the walls of the groove. A range of intermolecular hydrophobic and **hydrogen-bonding** interactions account for the sequence specific recognition in the complex. These include critical intermolecular contacts between the iodine and sulfur atoms of the thiobenzoate ring of the drug with the exposed exocyclic amino protons of the 5' and 3'-guanine **bases**, respectively, of the A-G-G-A segment on the DNA. The bound aryltetrasaccharide in turn positions the enediyne ring deep in the minor groove such that the pro-radical carbon centers of the enediyne are proximal to their anticipated proton abstraction sites. Specifically, the pro-radical C-3 and C-6 atoms are aligned opposite the abstractable H-5' (pro-S) and H-4' protons on partner strands across the minor groove, respectively, in the complex. The DNA duplex is right-handed with Watson-Crick **base**-pairing in the complex. The helix exhibits a B-DNA type minor groove width at the aryltetrasaccharide binding-site while there is widening of the groove at the adjacent enediyne binding-site in the complex. The DNA helix exhibits localized perturbations at the binding-site as reflected in imino proton complexation shifts and specific altered sugar pucker geometrics associated with complex formation. Sequence-specific binding of calicheamicin gamma 1I to the (T-C-C-T).(A-G-G-A) containing DNA hairpin duplex is favored by the **complementarity** of the fit through hydrophobic and **hydrogen-bonding** interactions between the drug and the floor and walls of the minor groove of a minimally perturbed DNA helix.

11/3,AB/14 (Item 14 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

08714122 96263414
Antisense strategies and therapeutic applications [published erratum

appears in Am J Health Syst Pharm 1996 Feb 1;53(3):325]
Putnam DA
Department of Pharmaceutics and Pharmaceutical Chemistry, University of Utah, Salt Lake City, UT 84112, USA.
American journal of health-system pharmacy (UNITED STATES) Jan 15 1996, 53 (2) p151-60; quiz 182-3, ISSN 1079-2082 Journal Code: CBH
Contract/Grant No.: GM08393, GM, NIGMS .
Languages: ENGLISH
Document type: JOURNAL ARTICLE; REVIEW; REVIEW, TUTORIAL

The concepts underlying the antisense approach to disease therapy are discussed, and potential applications are examined. Antisense therapeutic agents bind to DNA or RNA sequences, blocking the synthesis of cellular proteins with unparalleled specificity. Transcription and translation are the two processes with which the agents interfere. There are three major classes of antisense agents: antisense sequences, commonly called antisense oligonucleotides; antigene sequences; and ribozymes. Antisense sequences are derivatives of **nucleic acids** that hybridize cytosolic messenger RNA (mRNA) sense strands through **hydrogen bonding** to **complementary nucleic acid bases** . Antigene sequences hybridize double-stranded DNA in the nucleus, forming triple helixes. Ribozymes, rather than inhibiting protein synthesis simply by binding to a single targeted mRNA, combine enzymatic processes with the specificity of antisense **base** pairing, creating a molecule that can incapacitate multiple targeted mRNAs. Antisense therapeutic agents are being investigated in vitro and in vivo for use in treating human immunodeficiency virus infection, hepatitis B virus infection, herpes simplex virus infection, papillomavirus infection, cancer, restenosis, rheumatoid arthritis, and allergic disorders. Although many results are preliminary, some are promising and have led to clinical trials. A major goal in developing methods of delivering antisense agents is to reduce their susceptibility to nucleases while retaining their ability to bind to targeted sites. **Modification** of the phosphodiester linkages in oligonucleotides can lend the sequences enzymatic stability without affecting their binding capacities. Carrier systems designed to protect the antisense structure and improve passage through the cell membrane include liposomes, water-soluble polymers, and nanoparticles. The pharmacokinetics of antisense agents are under investigation. Antisense therapeutic agents have the potential to become an integral part of medicinal regimens.

11/3,AB/15 (Item 15 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

08679310 95034796
Structural characterization of two interchangeable conformations of a 2-aminofluorene-**modified** DNA oligomer by NMR and energy minimization.
Eckel LM; Krugh TR
Department of Chemistry, University of Rochester, New York 14627.
Biochemistry (UNITED STATES) Nov 22 1994, 33 (46) p13611-24, ISSN 0006-2960 Journal Code: A0G
Contract/Grant No.: CA35251, CA, NCI
Languages: ENGLISH
Document type: JOURNAL ARTICLE

One- and two-dimensional NMR spectroscopy and energy minimization calculations were used to investigate the conformation of a 2-aminofluorene- (AF-) **modified** model human c-H-ras1 protooncogene codon 61 deoxyoligonucleotide duplex, d(C1-A2-C3-C4-A5- [AF-G6]-G7-A8-A9-C10).-d(G11-T12-T13-C14-C15-T16 -G17-G18-T19-G20), in which the AF adduct is located at the third **base** of codon 61 with cytosine as the **complementary** nucleotide. Two interchangeable conformations of the AF-**modified** duplex, referred to as the external-AF conformation and the inserted-AF conformation, were determined from the NMR data. An analysis of the coalescence of resonances led to the estimation that the chemical exchange lifetime is greater than 3 ms but less than 20 ms at 30

degrees C, p[redacted]. In the external-AF conformation, Watson-Crick **base** -pair formati[redacted] is observed for all 10 **comp[redacted]entary** nucleotides, including the AF-G6.C15 **base** pair. In the inserted-AF conformation, 9 of the 10 **complementary bases** form Watson-Crick **base** pairs; the AF-G6 imino proton exhibits no evidence of **hydrogen bond** formation with its **complementary** cytosine. Several NOEs between aminofluorene protons and DNA protons show that the AF moiety in the inserted-AF conformation stacks between the adjacent A5.T16 and G7.C14 **base** pairs. Solvated energy minimization calculations using distance restraints obtained from NOESY data at 2 degrees C with a 100-ms mixing time were performed to obtain representative structures of the external-AF and inserted-AF conformations. The external-AF conformer has the AF moiety protruding out of the major groove of a relatively unperturbed DNA duplex, leaving intact Watson-Crick **base** pairing for the AF-G6.C15 **bases** . Thus, the external-AF conformer may represent a visualization of a conformation that allows faithful replication. The inserted-AF conformer has the AF moiety stacked within the DNA helix, breaking the Watson-Crick **base** pairing of the **modified** guanine and its **complementary** cytosine and displacing the guanine and cytosine into the grooves. We label the inserted-AF conformer as a premutagenic conformation to reflect the displacement of the **modified** guanine. Interconversion between the structurally distinct external-AF and inserted-AF conformers takes place on a time scale of the same order as DNA replication. We have labeled this interconversion as a mutagenic switch to highlight a possible conformational equilibrium that may be important in replication.

11/3,AB/16 (Item 16 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

08607828 96032632
The role of 2'-hydroxyl groups in an RNA-protein interaction.
Baidya N; Uhlenbeck OC
Department of Chemistry and Biochemistry, University of Colorado, Boulder 80309-0215, USA.
Biochemistry (UNITED STATES) Sep 26 1995, 34 (38) p12363-8, ISSN 0006-2960 Journal Code: A0G
Contract/Grant No.: GM35772, GM, NIGMS
Languages: ENGLISH
Document type: JOURNAL ARTICLE

The role of the 2'-hydroxyl group in RNA--protein interaction has been investigated using MS2 coat protein and its hairpin RNA operator as a model system. Derivatives of the MS2 translational operator were prepared where individual riboses were replaced by deoxyribose and their binding affinities to MS2 coat protein were determined. Only 1 (U-5) out of 15 positions tested reduced protein affinity by 1.6 kcal/mol. A variety of other 2'-**modifications** were tested at this position to understand the role of this particular 2'-hydroxyl group. Normal binding of the U-NH2 variant and weaker binding of the U-O-methyl variant are consistent with the ability of these functional groups to provide a **hydrogen bond** donor. This is also supported by recent crystallographic data which indicate a possible interaction between the 2'-hydroxyl of U-5 and the carboxylate group of glutamate 63 [Valeg.ANG.ard et al. (1994) Nature 371, 623-626]. **Complementary** experiments introducing riboses into a DNA hairpin confirm the putative protein contact, and also identify a requirement for riboses in the two upper **base** pairs of the hairpin. Several arguments suggest these riboses are required to maintain an A-form helix in this region of the binding site. A minimum requirement of four 2'-hydroxyl groups for wild-type coat protein binding has been determined, one of which is at the -5 position and other three in the upper stem in any combination.(ABSTRACT TRUNCATED AT 250 WORDS)

11/3,AB/17 (Item 17 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
(c) format only 2000 Dialog Corporation. All rts. reserv.

08550255 96072774
Structural alignments of (+)- and (-)-trans-anti-benzo[a]pyrene-dG adducts positioned at a DNA template-primer junction.
Cosman M; Hingerty BE; Geacintov NE; Broyde S; Patel DJ
Cellular Biochemistry and Biophysics Program, Memorial Sloan Kettering Cancer Center, New York, New York 10021, USA.
Biochemistry (UNITED STATES) Nov 21 1995, 34 (46) p15334-50, ISSN 0006-2960 Journal Code: A0G
Contract/Grant No.: CA-46533, CA, NCI; CA-20851, CA, NCI; CA-28038, CA, NCI
Languages: ENGLISH
Document type: JOURNAL ARTICLE
The structural features of a chemically **modified** DNA template strand may promote error-prone DNA synthesis during replication. The resulting higher incidence of mutations, in turn, can eventually lead to tumor initiation. Structural insights into this process can be monitored by studying chemically **modified** **base** adducts of defined stereochemistry positioned site-specifically at a single strand--duplex template--primer junction. We have used a NMR-molecular mechanics approach to obtain the solution conformations of the covalent adducts derived from trans additions at the [BP]C10 position of the highly tumorigenic (+)-anti-benzo[a]pyrene diol epoxide [(+)-anti-BPDE] and nontumorigenic (-)-anti-benzo-[a]pyrene diol epoxide [(-)-anti-BPDE] to the N2 position of guanine [(+) and (-)-trans-anti-[BP]dG, respectively] in the d(A1-A2-C3-[BP]G4-C5-T6-A7-C8-C9-A10-T11-C12-C13).d (G14-G15-A16-T17-G18-G19-T20-A 21-G22) 13/9-mer DNA sequence. The **modified** 13-mer strand constitutes the template strand, while the **complementary** 9-mer strand constitutes a primer which has been synthesized from the 3'-end of the template toward the 5'-end up to the **base** preceding, but not including, the **modified** guanine. The **modified** guanine (denoted by [BP]dG4) is positioned at the junction site between the single-stranded and duplex segments. Structural features of the (+)-trans-anti-[BP]dG 13/9-mer have been determined by incorporating proton--proton distances defined by lower and upper bounds deduced from NOESY spectra as restraints in molecular mechanics computations in torsion angle space. The 3'-side duplex segment retains a minimally perturbed B-DNA conformation with all nine **base** pairs in Watson--Crick **hydrogen-bonded** alignments. Conformational heterogeneity is detected at the single-stranded d(A1-A2-C3) segment located 5' to the **modified** (+)-trans-anti-[BP]dG lesion which contrasts with an unperturbed alignment of these same residues in the unmodified control 13/9-mer. The **modified** guanine adopts a syn glycosidic torsion angle, is displaced into the major groove, and no longer stacks over the adjacent dC5.dG22 **base** pair. Such a **base** displacement is accompanied by stacking of one face of the pyrenyl ring with the dC5.dG22 **base** pair located on the duplex segment proximate to the **modified** guanine, while the other face of BP is exposed to solvent.(ABSTRACT TRUNCATED AT 400 WORDS)

11/3,AB/18 (Item 18 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
(c) format only 2000 Dialog Corporation. All rts. reserv.

08421773 96027474
NMR solution structure of a nonanucleotide duplex with a dG mismatch opposite a 10S adduct derived from trans addition of a deoxyadenosine N6-amino group to (+)-(7R,8S,9S,10R)-7,8-dihydroxy-9,10-epoxy-7,8,9,10-tetrahydrobenzo[a]pyrene: an unusual syn glycosidic torsion angle at the **modified** dA.
Yeh HJ; Sayer JM; Liu X; Altieri AS; Byrd RA; Lakshman MK; Yagi H; Schurter EJ; Gorenstein DG; Jerina DM

NIDDK, National Institutes of Health, Bethesda, Maryland 20892, USA.
Biochemistry (UNITED STATES) Oct 17 1995, 34 (41) p13570-81, ISSN
0006-2960 Journal Code: A0G
Contract/Grant No.: NO1-CO-46000, CO, NCI
Languages: ENGLISH
Document type: JOURNAL ARTICLE

A nonanucleotide, d(G1G2T3C4[BaP]A5C6G7A8G9), in which (+)-(7R,8S,9S,10R)-7,8-dihydroxy-9,10-epoxy-7,8,9,10- tetrahydrobenzo[a]pyrene (7-hydroxyl group and epoxide oxygen are trans) is covalently bonded to the exocyclic N6-amino group of deoxyadenosine (dA5) through trans addition at C10 of the epoxide (to give a 10S adduct) has been synthesized. The solution structure of the duplex, d(G1G2T3C4[BaP]A5C6G7A8G9).d(C10T11C12G13G14G15A16C17C18+ ++), containing a dG mismatch opposite the **modified** dA (designated 10S-[BaP]dA.dG 9-mer duplex) has been investigated using a combination of 1D and 2D (including COSY, PECOSY, TOCSY, NOESY, and indirect detection of 1H-31P HETCOR) NMR spectroscopies. The NMR results together with restrained molecular dynamics/energy minimization calculations show that the **modified** dA5 adopts a syn glycosidic torsion angle whereas all other nucleotide residues adopt anti glycosidic torsion angles. The sugar ring of dA5 is in the C3'-endo conformation, and the sugar rings of the other residues are in the C2'-endo conformation. The hydrocarbon attached at dA5 orients toward the 3' end of the **modified** strand (i.e., dC6 direction) and intercalates between and parallel to **bases** of dG13 and dG14 of the **complementary** strand directly opposite dC6 and dA5, respectively. The edge of the hydrocarbon bearing H11 and H12 is positioned between the imino protons of dG13 and dG14 in the interior of the duplex, whereas H4 and H5 at the opposite edge are positioned near the sugar H1' and H2" protons of dG13 and facing the exterior of the duplex. The mismatched AG **base** pair is stabilized by dAsyn-dGanti **base** pairing in which the imino proton and the O6 of dG14 are **hydrogen bonded** to N7- and the single N6-amino proton, respectively, of the **modified** dA5. The **modified** DNA duplex remains in a right-handed helix, which bends at the site of intercalation about 20 to 30 degrees away from the helical axis and toward the direction of the **modified** strand.

11/3,AB/19 (Item 19 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07987912 94347761
High-field NMR and restrained molecular modeling studies on a DNA heteroduplex containing a **modified** apurinic abasic site in the form of covalently linked 9-aminoellipticine.
Singh MP; Hill GC; Peoc'h D; Rayner B; Imbach JL; Lown JW
Department of Chemistry, University of Alberta, Edmonton, Canada.
Biochemistry (UNITED STATES) Aug 30 1994, 33 (34) p10271-85, ISSN
0006-2960 Journal Code: A0G
Languages: ENGLISH
Document type: JOURNAL ARTICLE

Two-dimensional NMR methods were used to model the possible solution structure of an intercalative complex of 9-aminoellipticine (Aell), a polycyclic pyridocarbazolamine, covalently bound to an apurinic ring-opened deoxyribose site of a duplex DNA fragment in the reduced Schiff **base** form. The required oligonucleotide single strand containing covalently attached aminoellipticine was obtained by reductive amination in the presence of sodium cyanoborohydride. The combined NMR-energy minimization methods were employed to refine the model structures of two distinct forms, intrahelical and extrahelical, of a control 9-mer duplex DNA, d(CGTG.dr.GTGC).d(GCACTCACG), which contains an apurinic site positioned opposite a dT residue on the **complementary** strand. The model structure of an aminoellipticine conjugate with the same DNA sequence, derivatized via the aforementioned covalent attachment, was also obtained by incorporating intermolecular drug-DNA, and intra- and internucleotide

NOE-derived proton-proton distance estimates as restraints in energy minimization routines. The indole ring system of aminoellipticine, which is inserted at the apurinic site, intercalates between and is parallel to flanking GC **base** pairs. The pyridinic ring of aminoellipticine, in protonated form, also stacks between cytidine and thymidine **bases** on the **complementary** strand, which is consistent with the observation that the normal sequential NOE connectivity at the 5'-C13-T14 step is broken and indeed diverted through the ellipticine moiety, e.g., C13-Aell-T14 connectivities through the Aell-H4/C5Me protons. Interestingly, the partial stacking of the pyridinic ring is observed only between the 5'-CT step vs an adjacent 5'-TC step, owing to inherently weak stacking interactions associated with the former. In the absence of any potential groups that can participate in electrostatic or **hydrogen-bonding** interactions with the **nucleic acid**, pi-pi stacking and hydrophobic contacts at the intercalation site appear to be the important factors in determining stability and conformation of the aminoellipticine-DNA conjugate. Stacking interactions in such a bistranded intercalative complexation of aminoellipticine apparently govern the formation of a single intrahelical form of a right-handed B-type DNA duplex. The overall structural features lead us to propose working models for an enzyme-like DNA cleavage activity of 9-aminoellipticine and the observed inhibition of the AP endonuclease-dependent DNA excision-repair pathway.

11/3,AB/20 (Item 20 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07928617 94254097
A parallel DNA triplex as a model for the intermediate in homologous recombination.
Zhurkin VB; Raghunathan G; Ulyanov NB; Camerini-Otero RD; Jernigan RL
Laboratory of Mathematical Biology, NCI, NIH, Bethesda, MD 20892.
Journal of molecular biology (ENGLAND) Jun 3 1994, 239 (2) p181-200,
ISSN 0022-2836 Journal Code: J6V
Languages: ENGLISH
Document type: JOURNAL ARTICLE
Parallel DNA triplexes considered to be putative intermediates in homologous recombination, are studied by means of theoretical conformational analysis. These triplexes are denoted as the R-form DNA. Two types of triplexes are analyzed: extended R-form DNA, modeling the triple standard structure, created transiently in the presence of recombination proteins (e.g. RecA); and collapsed R-form, obtained after deproteinization. These structures are stereochemically possible for any arbitrary sequence and have the following properties: (1) the third, R-strand, is parallel to the identical duplex strand and is located in the major groove of the duplex; (2) positions of all four **bases** in the R-strand are nearly isomorphic; (3) the proposed triplets are consistent with the chemical **modification** data for deproteinized DNA; we suggest, however, that they are the same in the RecA-DNA complex as well. Since the patterns of charges on each **base** of the R-strand are strictly **complementary** to the charges of the homologous Watson-Crick (WC) pair in the major groove, we propose that the selection of the homologous sequence may occur through these **complementary** electrostatic interactions (electrostatic recognition code). We demonstrate that in the collapsed triplex with a rise of about 3.4 A, the **bases** from the third R-strand can be inclined and interact with two WC **base**-pairs simultaneously, which could lead to recognition errors. These mispairings are unlikely in the extended triplex. Therefore, we speculate that a functional role of the extended and underwound DNA structure, transiently formed in the complex with RecA protein, is to obviate such errors and increase the stringency of recognition. In other words, RecA plays the role of a DNA chaperone facilitating the recognition of the single stranded DNA and the duplex. Finally, we show that the

proposed isomorphic triplets are conformationally advantageous for strand exchange.

11/3,AB/21 (Item 21 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07815861 93237235
Identification of specific contacts in T3 RNA polymerase-promoter interactions: kinetic analysis using small synthetic promoters.
Schick C; Martin CT
Program in Molecular and Cellular Biology, University of Massachusetts, Amherst 01003.
Biochemistry (UNITED STATES) Apr 27 1993, 32 (16) p4275-80, ISSN 0006-2960 Journal Code: A0G
Languages: ENGLISH
Document type: JOURNAL ARTICLE
The T7, T3, and SP6 RNA polymerases recognize very similar, yet distinct, promoter sequences. The high homology among the promoter sequences suggests that differential promoter recognition must derive from relatively small changes in the protein. Steady-state kinetic analyses of transcription from the T3 consensus promoter and from promoters **modified** in the region critical to specific recognition reveal details concerning which functional groups contribute to this recognition. **Modifications** include **base** pair substitutions, single **base** substitutions (mismatches), and simple functional group **modifications** at unique sites in the promoter. The results show that T3 RNA polymerase recognizes the amino group on the nontemplate cytidine in the major groove at position -10, while the identity of the **base** on the template strand is less critical to binding. In contrast, recognition at position -11 allows a greater range of **modifications** and seems to have a more complex recognition. The results do not seem to be consistent with a single recognition contact at this position; however, some groups may be ruled out as simple recognition contacts. While major groove **modifications** weaken binding at positions -10 and -11, the removal of an exocyclic amino group from the minor groove at either position does not disrupt binding, further supporting a model for promoter recognition in which the enzyme binds to one face of closed duplex DNA in this region. The effects of these changes in the DNA structure on the kinetics of initiation are compared to **complementary** results from the T7 system..

11/3,AB/22 (Item 22 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07797728 93221710
Conformational isomerizations of poly(dA-dT) are dramatically influenced by a substitution of a minor amount of adenine by purine or amino2purine.
Vorlickova M; Sagi J; Szabolcs A; Ebinger K; Fellegvari I; Kypr J
Institute of Biophysics, Czechoslovak Academy of Sciences, Brno.
Journal of biomolecular structure & dynamics (UNITED STATES) Feb 1993, 10 (4) p681-92, ISSN 0739-1102 Journal Code: AH2
Languages: ENGLISH
Document type: JOURNAL ARTICLE
We have synthesized poly(dA,dPu-dT) and poly(dA,n2dPu-dT) containing, respectively, 5.7% of purine and 7.4% of amino2purine in place of adenine to demonstrate that these apparently negligible perturbations of the primary structure have dramatic consequences for the polynucleotide conformational isomerizations. The replacement of adenine by amino2purine, preserving the number of **hydrogen bonds** between the **complementary bases**, has a stronger effect on the polynucleotide conformational isomerizations than the replacement with purine that is bound only by a single **hydrogen bond** to thymine.

Nevertheless, poly(dA,dPu-dT) forms a more thermostable duplex than poly(dA,n2dPu-dT). Furthermore the few amino2purines in poly(dA,n2dPu-dT) inhibit its isomerization into X-DNA, stabilize but **modify** A-DNA and stabilize Z-DNA. Kinetics of the B-Z transition of poly(dA,n2dPu-dT) is fast to indicate that the amino groups in the double helix minor groove substantially decrease the kinetic barrier between B- and Z-DNA. On the other hand, the replacement of adenine by purine destabilizes both Z-DNA and A-DNA, and the destabilization of X-DNA is weaker than with amino2purine. A-form and B-form perhaps coexist in poly(dA,dPu-dT) at high concentrations of ethanol.

11/3,AB/23 (Item 23 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07510239 93192188
Structural characterization of an N-acetyl-2-aminofluorene (AAF) **modified** DNA oligomer by NMR, energy minimization, and molecular dynamics.
O'Handley SF; Sanford DG; Xu R; Lester CC; Hingerty BE; Broyde S; Krugh TR
Department of Chemistry, University of Rochester, New York 14627.
Biochemistry (UNITED STATES) Mar 16 1993, 32 (10) p2481-97, ISSN 0006-2960 Journal Code: A0G
Contract/Grant No.: CA35251, CA, NCI; CA28038, CA, NCI; RR03317, RR, NCRR ; +
Languages: ENGLISH
Document type: JOURNAL ARTICLE
An N-acetyl-2-aminofluorene (AAF) **modified** deoxyoligonucleotide duplex, d(C1-C2-A3-C4-[AAF-G5]-C6-A7-C8-C9).d(G10-G11-T12-G13-C14-++ +G15-T16-G17-G18), was studied by one- and two-dimensional NMR spectroscopy. Eight of the nine **complementary** nucleotides form Watson-Crick **base** pairs, as shown by NOEs between the guanine imino proton and cytosine amino protons for G.C **base** pairs or by an NOE between the thymine imino proton and adenine H2 proton for A.T **base** pairs. The AAF-G5 and C14 **bases** show no evidence of **complementary** **hydrogen** **bond** formation to each other. The AAF-G5 **base** adopts a syn conformation, as indicated by NOEs between the G5 imino proton and the A3-H3' and A3-H2'/H2" protons and by NOEs between the fluorene-H1 proton of AAF and the G5-H1' or C6-H1' proton. The NOEs from the C4-H6 proton to C4 sugar protons are weak, and thus the glycosidic torsion angle in this nucleotide is not well defined by these NMR data. The remaining **bases** are in the anti conformation, as depicted by the relative magnitude of the H8/H6 to H2' NOEs when compared to the H8/H6 to H1' NOEs. The three **base** pairs on each end of the duplex exhibit NOEs characteristic of right-handed B-form DNA. Distance restraints obtained from NOESY data recorded at 32 degrees C using a 100-ms mixing time were used in conformational searches by molecular mechanics energy minimization studies. The final, unrestrained, minimum-energy conformation was then used as input for an unrestrained molecular dynamics simulation. Chemical exchange cross peaks are observed, and thus the AAF-9-mer exists in more than a single conformation on the NMR time scale. The NMR data, however, indicate the presence of a predominant conformation (> or = 70%). The structure of the predominant conformation of the AAF-9-mer shows stacking of the fluorene moiety on an adjacent **base** pair, exhibiting features of the **base** -displacement [Grunberger, D., Nelson, J. H., et al. (1970) Proc. Natl. Acad. Sci. U.S.A. 66, 488-494] and insertion-denaturation models [Fuchs, R.P.P., & Daune, M. (1971) FEBS Lett. 14, 206-208], while the distal ring of the fluorene moiety protrudes into the minor groove.

11/3,AB/24 (Item 24 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

07379502 92144014

The mechanism of recognition of templates by DNA polymerases from pro- and eukaryotes as revealed by affinity **modification** data.

Kolocheva TI; Nevinsky GA; Levina AS; Khomov VV; Lavrik OI

Novosibirsk Institute of Bioorganic Chemistry, Siberian Division of the Academy of Sciences of the USSR.

Journal of biomolecular structure & dynamics (UNITED STATES) Aug 1991, 9 (1) p169-86, ISSN 0739-1102 Journal Code: AH2

Languages: ENGLISH

Document type: JOURNAL ARTICLE

Pt(2+)-containing derivatives of oligodeoxyribonucleotides were used to evaluate the ligand affinity to the template sites of Klenow fragment of DNA polymerase I from E. coli and DNA polymerase alpha from human placenta. The values of Kd and Gibb's energy (delta G degree) for the complexes of oligodeoxyribonucleotides and their derivatives with the template sites of these enzymes were determined from the effects protecting the enzyme from inactivation by Pt(2+)-containing oligonucleotides. Kd and delta G degree values of the complexes made by DNA polymerases and orthophosphate, triethylphosphate, d(pC)n, d(pT)n, d(pG)n, d(pA)n (where n = 1-25), heterooligonucleotides of various length and structure, and oligothymidylates with partially and completely ethylated internucleotide phosphates were evaluated. The obtained data enabled us to suggest 19-20 mononucleotide units of the template to interact with the protein. Only one template internucleotide phosphate forms a Me(2+)-dependent electrostatic contact (delta G = -1.1...-1.7 kcal/mol) and a **hydrogen bond** (delta G = -4.4...-4.9 kcal/mol) with the enzyme. It is likely that the mononucleoside units of the template form hydrophobic contacts with the enzymes. The efficiency of such interaction changes with the hydrophobicity of the **bases** : C less than T less than G approximately A. For both homo- and heterooligonucleotides the contributions of nucleoside units to the affinity of the templates to the enzymes is due to the **complementary** interactions with the primers. A hypothetical model for the template-primer interaction with DNA polymerases is suggested.

11/3,AB/25 (Item 25 from file: 155)

DIALOG(R)File 155:MEDLINE(R)

06931537 92107985

How does RNase H recognize a DNA.RNA hybrid?

Nakamura H; Oda Y; Iwai S; Inoue H; Ohtsuka E; Kanaya S; Kimura S; Katsuda C; Katayanagi K; Morikawa K; et al.

Protein Engineering Research Institute, Osaka, Japan.

Proceedings of the National Academy of Sciences of the United States of America (UNITED STATES) Dec 15 1991, 88 (24) p11535-9, ISSN 0027-8424 Journal Code: PV3

Languages: ENGLISH

Document type: JOURNAL ARTICLE

The mechanism of RNase H substrate recognition is proposed from a model of a chemically **modified** DNA.RNA hybrid Escherichia coli RNase H complex. Site-directed mutagenesis of the enzyme and substrate titration observed by heteronuclear two-dimensional NMR spectra have been carried out. A model complex has been built, **based** on free structures of the enzyme and the substrate independently determined by x-ray crystallography and NMR distance geometry, respectively. In addition to steric and electrostatic **complementarities** between the molecular surfaces of the enzyme and the minor groove of the hybrid in the model, putative **hydrogen bonds** between the polar groups in the enzyme and 2'-oxygens of the RNA strand of the hybrid fix the hybrid close to the active site of the enzyme. The enzymatic activities of the mutant proteins and the changes in NMR spectra during the course of substrate titration are consistent with the present model. Moreover, the specific cleavage of the

RNA strand in [redacted]RNA hybrids can be explained [redacted]well as cleavage modes in **modified** hetero[redacted]plexes. A mechanism of enzymati[redacted]ction is proposed.

11/3,AB/26 (Item 26 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

06741833 91321632
Study of the structural-energy aspects of **complementary**-addressed **modifications** of **nucleic acids** by reactive oligonucleotide derivatives having a 4-[N-methyl-N-(2-chloroethyl)amino[benzylidene group at the 3'end by a molecular mechanics method]
Issledovanie metodom molekuliarnoi mekhaniki strukturno- energeticheskikh aspektov komplementarno-adresovannoi **modifikatsii** nukleinovykh kislot reaktsionnosposobnymi proizvodnymi oligonukleotidov, nesushchikh na 3'-kontse 4-[N-metil-N-(2-khloro- etil)amino[benzilidenovyiu gruppirovku.
Vorob'ev IuN
Bioorganicheskaia khimiia (USSR) Feb 1991, 17 (2) p211-22, ISSN 0132-3423 Journal Code: 9Z8
Languages: RUSSIAN Summary Languages: ENGLISH
Document type: JOURNAL ARTICLE English Abstract
Calculations of probabilities of the **complementary** addressed **modification** of a target **nucleic acid** by derivatives of oligonucleotides carrying a 4-[N-(2-chloroethyl)-N-methyl]aminobenzylidene group attached to the 3'-end (3'-BDO) have been made. The results show that the **complementary** complex of a target [redacted]NA with 3'-BDO having R-configuration of carbon atom of the dioxalane ring is more stable than the complex including the S-stereoisomer. The S- and R-epimeres of 3'-BDO have essentially different positional abilities for alkylation of the target. The R-epimer alkylates best of all the third **base** of the target NA from terminal **complementary** pair of the complex. The S-epimer has another site the most sensitive to alkylation, which is a terminal **complementary base** of the target NA or the adjacent nonpaired **base**. Formation of the alkylation complexes are accompanied with a loss or a breakdown of **hydrogen bonds** in the terminal **complementary base** pair, thus decreasing the efficiency of alkylation. The modelling results are considered along with experimental data on **modification** which therefore can be interpreted on the fundamental structural level.

11/3,AB/27 (Item 27 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

06626280 90275214
NMR studies of an exocyclic 1,N2-propanodeoxyguanosine adduct (X) located opposite deoxyadenosine (A) in DNA duplexes at basic pH: simultaneous partial intercalation of X and A between stacked **bases**.
Kouchakdjian M; Eisenberg M; Live D; Marinelli E; Grollman AP; Patel DJ
Department of Biochemistry and Molecular Biophysics, College of Physicians and Surgeons, Columbia University, New York, New York 10032.
Biochemistry (UNITED STATES) May 8 1990, 29 (18) p4456-65, ISSN 0006-2960 Journal Code: A0G
Contract/Grant No.: CA-49982, CA, NCI; CA-47995, CA, NCI
Languages: ENGLISH
Document type: JOURNAL ARTICLE
The NMR parameters for the 1,N2-propanodeoxyguanosine (X) opposite deoxyadenosine positioned in the center of the **complementary** d(C1-A2-T3-G4-X5-G6-T7-A8-C9).d(G10-T11-A12-C13-A14-C15-A 16-T17-G18) X.A 9-mer duplex are pH dependent. A previous paper established protonated X5(syn).A14(anti) pairing in the X.A 9-mer duplex at pH 5.8 [Kouchakdjian, M., Marinelli, E., Gao, X., Johnson, F., Grollman, A., & Patel, D. J. (1989) Biochemistry 28, 5647-5657]; this paper focuses on the pairing

alignment at the lesion site at pH 8.9. The observed NOEs between specific exocyclic CH2 protons and both the imino proton of G6 and the sugar H1' protons of C13 and A14 establish that X5 is positioned toward the G6.C13 **base** pair with the exocyclic ring directed between C13 and A14 on the partner strand. The observed NOE between the H2 proton of A14 and the imino proton of G4, but not G6, establishes that A14 at the lesion site is directed toward the G4.C15 **base** pair. NOEs are detected between all exocyclic CH2 protons of X5 and the H2 proton of A14, confirming that both X5 and A14 are directed toward the interior of the helix. The X5(anti).A14(anti) alignment at pH 8.9 is accommodated within the helix with retention of Watson-Crick pairing at flanking G4.C15 and G6.C13 **base** pairs. The energy-minimized conformation of the (G4-X5-G6).(C13-A14-C15) segment at pH 8.9 establishes that X5 and A14 are directed into the helix, partially stack on each other, and are not stabilized by intermolecular **hydrogen bonds**. The X5 **base** is partially intercalated between C13 and A14 on the unmodified strand, while A14 is partially intercalated between G4 and X5 on the **modified** strand. This results in a larger separation between the G4.C15 and G6.C13 **base** pairs flanking the lesion site in the basic pH conformation of the X.A 9-mer duplex. The midpoint of the transition between the protonated X5(syn).A14(anti) and X5(anti).A14(anti) conformations occurs at pH 7.6, establishing an unusually high pKa for protonation of the A14 ring opposite the X5 exocyclic adduct site. Thus, the interplay between hydrophobic and **hydrogen-bonding** contributions modulated by pH defines the alignment of 1,N2-propanodeoxyguanosine opposite deoxyadenosine in the interior of DNA helices.

11/3,AB/28 (Item 28 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

06534202 91104846
Determination of the major tautomeric form of the covalently **modified** adenine in the (+)-CC-1065-DNA adduct by 1H and 15N NMR studies.
Lin CH; Hurley LH
Drug Dynamics Institute, College of Pharmacy, University of Texas, Austin 78712.
Biochemistry (UNITED STATES) Oct 16 1990, 29 (41) p9503-7, ISSN 0006-2960 Journal Code: A0G
Contract/Grant No.: CA-49751, CA, NCI
Languages: ENGLISH
Document type: JOURNAL ARTICLE
CC-1065 is an extremely potent antitumor antibiotic produced by Streptomyces zelensis. The potent cytotoxic effects of the drug are thought to be due to the formation of a covalent adduct with DNA through N3 of adenine. Although the covalent linkage sites between (+)-CC-1065 and DNA have been determined, the tautomeric form of the covalently **modified** adenine in the (+)-CC-1065-DNA duplex adduct was not defined. A [6-15N]deoxyadenosine-labeled 12 **base** pair non-self-**complementary** oligomer, d(GGCGGAGTT*AGG).d(CCTAACTCCGCC) (asterisk indicates 15N-labeled **base**), containing the (+)-CC-1065 most preferred binding sequence 5'AGTTA, was synthesized and **modified** with (+)-CC-1065. This [6-15N]deoxyadenosine-labeled 12-mer duplex adduct was then studied by 1H and 15N NMR. One-dimensional NOE difference and two-dimensional NOESY 1H NMR experiments on the nonisotopically labeled 12-mer duplex adduct demonstrate that the 6-amino protons of the covalently **modified** adenine exhibit two signals at 9.19 and 9.08 ppm. Proton NMR experiments on the [6-15N]deoxyadenosine-labeled 12-mer duplex adduct show that the two resonance signals for adenine H6 observed on the nonisotopically labeled duplex adduct were split into doublets by the 15N nucleus with coupling constants of 91.3 Hz for non-**hydrogen-bonded** and 86.8 Hz for **hydrogen-bonded** amino protons. Parallel 15N NMR experiments on the [6-15N]deoxyadenosine-labeled

(+)-CC-1065-12-[redacted] duplex adduct show a triplet like signal around -276.9 ppm and coupling constants of 91.5 and 85.6 Hz [redacted] BSTRACT TRUNCATED AT 250 WORDS)

11/3,AB/29 (Item 29 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
(c) format only 2000 Dialog Corporation. All rts. reserv.

06241365 89335856
Protein-**nucleic acid** interactions in reactions catalyzed by eukaryotic and prokaryotic DNA-polymerases]
Belok-nukleinovye vzaimodeistviia v reaktsiiakh, kataliziruemykh DNK-polimerazami eukariot i prokariot.
Lavrik OI; Nevinskii GA
Biokhimiia (USSR) May 1989, 54 (5) p757-64, ISSN 0320-9725
Journal Code: A28
Languages: RUSSIAN Summary Languages: ENGLISH
Document type: JOURNAL ARTICLE English Abstract
A new method of estimation of dissociation constants for ligands and free energies of its binding **based** on the affinity **modification** of active centers in the presence of competitive ligands was developed. This method is designed for the analysis of protein-**nucleic acid** interactions in template systems. Deoxyoligoribonucleotides containing the reactive residue of cis-aquadihydroxydiaminoplatinum (II) and oligonucleotides ethylated at phosphate groups were used for the study of interactions of human placental DNA-polymerase alpha and the Klenow fragment of DNA-polymerase I from E. coli with templates and primers. A model was constructed which postulates the formation of a single Me2+-dependent electrostatic bond and of a **hydrogen bond** by one of template phosphates with the enzyme active center. Similar bonds form the basis for the enzyme interaction with the 3'-terminal phosphate group of the primer. Other monomeric units of the template are likely to interact with the enzyme by forming hydrophobic bonds. Other mononucleotide units of the primer are involved in **complementary** interactions with the template. The primer activity of dNMP and NMP in these systems has been demonstrated for the first time. The efficiency of dNMP, dNDP and dNTP interaction with DNA-polymerase was estimated from the affinity **modification** of the enzymes by dNTP and dNMP imidazolides. The key role of the template-primer interaction in the formation of the dNTP-binding site of DNA-polymerases was demonstrated. A significant contribution of dNTP gamma-phosphate to the template--dependent specific tuning of substrate dNTP was revealed.

11/3,AB/30 (Item 30 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
(c) format only 2000 Dialog Corporation. All rts. reserv.

06222318 89000969
Protein-**nucleic acid** interaction in reactions catalyzed with DNA polymerases.
Knorre DG; Lavrik OI; Nevinsky GA
Institute of Bioorganic Chemistry, Siberian Division of the Academy of Sciences, Novosibirsk, U.S.S.R.
Biochimie (FRANCE) May 1988, 70 (5) p655-61, ISSN 0300-9084
Journal Code: A14
Languages: ENGLISH
Document type: JOURNAL ARTICLE
The affinities of oligothymidylates and of some analogs for the template site, of a set of oligodeoxyribo- and oligoribonucleotides for the primer site, and of dNTPs and some analogs for the substrate sites of DNA polymerase I Klenow fragment and of human placenta DNA polymerase alpha were measured using them either as competitors of affinity **modification** or as substrates. The data obtained enable us to

hypothesize that the Me2+-dependent electrostatic contact and **hydrogen bond** of a single internucleotide phosphate and the hydrophobic interactions of the other nucleotide units determine the formation of oligonucleotide-template site complexes. Interaction of the primer's 3'-terminal hydroxy group and of the negatively charged adjacent phosphate with the enzyme, and Watson-Crick **base** pairing with the template are of crucial importance for the formation of the ternary enzyme-template-primer complex. dNTP and dNMP imidazolides inactivate enzymes via an affinity **modification** mechanism only in the presence of the template-primer complex. dNTP affinities exceed those of dNDPs and dNMPs, the enhancement being most significant for the substrate that is **complementary** to the template, thus suggesting the participation of the gamma-phosphate of dNTP in the substrate selection step.

11/3,AB/31 (Item 31 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

06069901 88163554
Base pair mismatches and carcinogen-**modified bases** in DNA: an NMR study of A.C and A.O4meT pairing in dodecanucleotide duplexes.
Kalnik MW; Kouchakdjian M; Li BF; Swann PF; Patel DJ
Department of Biochemistry and Molecular Biophysics, College of Physicians and Surgeons, Columbia University, New York, New York 10032.
Biochemistry (UNITED STATES) Jan 12 1988, 27 (1) p100-8, ISSN 0006-2960 Journal Code: A0G
Contract/Grant No.: CA-46533, CA, NCI
Languages: ENGLISH
Document type: JOURNAL ARTICLE
Structural features of A.C mismatches and A.O4meT pairs in the interior of oligodeoxynucleotide duplexes have been investigated by high-resolution two-dimensional proton NMR spectroscopy on the self-**complementary** d(C-G-C-A-A-G-C-T-C-G-C-G) duplex (designated A.C 12-mer) and and the self-**complementary** d(C-G-C-A-A-G-C-T-O4meT-G-C-G) duplex (designated A.O4meT 12-mer) containing A.C and A.O4meT pairs at identical positions four **base** pairs in from either end of and A.O4meT pairs at identical positions four **base** pairs in from either end of the duplex. Proton NMR shows that there are similar pH-dependent changes in the structure in the A.C 12-mer and A.O4meT 12-mer duplexes. Our studies have focused on the low-pH (pH 5.5) conformation where high-quality two-dimensional NOESY data sets were collected from the exchangeable and nonexchangeable protons in these duplexes. The spectral parameters for the A.C 12-mer and the A.O4meT 12-mer duplexes were very similar, indicating that they must have similar structures at this pH in aqueous solution. Both structures are right-handed double helices with all the **bases** adopting the normal anti configuration about the glycosidic bond. The same atoms are involved in **hydrogen-bond** pairing for the A.C mismatch and the A.O4meT pair, and these pairs have a similar spatial relationship to flanking **base** pairs.(ABSTRACT TRUNCATED AT 250 WORDS)

11/3,AB/32 (Item 32 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

05632627 90105453
Structure and dynamics of a fluorescent DNA oligomer containing the EcoRI recognition sequence: fluorescence, molecular dynamics, and NMR studies.
Nordlund TM; Andersson S; Nilsson L; Rigler R; Graslund A; McLaughlin LW
Department of Medical Biophysics, Karolinska Institutet, Stockholm, Sweden.
Biochemistry (UNITED STATES) Nov 14 1989, 28 (23) p9095-103, ISSN 0006-2960 Journal Code: A0G
Contract/Grant No.: 1 F06 TW01332, TW, FIC; CA-41368, CA, NCI; GM-37065,

GM, NIGMS
Languages: EN[redacted]SH
Document type: JOURNAL ARTICLE
The self-**complementary** DNA decamer duplex d(CTGAATTCAG)2 and its **modified** counterpart d(CTGA[2AP]TTCAG)2, where the innermost adenine (6-aminopurine) has been replaced with the fluorescent analogue 2-aminopurine (2AP), have been studied by fluorescence and NMR spectroscopy and simulated by molecular dynamics. Both decamers are recognized and cleaved by the EcoRI restriction endonuclease. 2D NMR results show that both decamers have a standard B-type conformation below 20 degrees C, though a disturbance exists to the 5' side of the 2AP site which may originate from increased local mobility. The fluorescence and fluorescence anisotropy decays of both decamers, as well as the one containing 2AP in only one chain, were studied as a function of temperature. The data show that the 2AP **base** exists in a temperature-dependent distribution of states and shows rapid motions, suggesting interconversion among these states on a time scale of about 10(-10) s. The integrated fluorescence of the decamer with 2AP in both chains shows a large increase around the helix melting temperature whereas the decamer with one 2AP shows only a mild increase, showing that the mixed helix has a different structural transition as sensed by the 2AP **base**. The data suggest a model of conformational states which have distinct fluorescence decay times. The various states may differ in the degree of **base** stacking. Fluctuations in the degree of stacking of the A or 2AP **base** are supported by molecular dynamics simulations, which additionally show that the 2AP-T or A-T **base** pair **hydrogen bonds** remain intact during these large motions.

11/3,AB/33 (Item 33 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

05300528 88163555
Base pair mismatches and carcinogen-**modified bases** in DNA: an NMR study of G.T and G.O4meT pairing in dodecanucleotide duplexes.
Kalnik MW; Kouchakdjian M; Li BF; Swann PF; Patel DJ
Department of Biochemistry and Molecular Biophysics, College of Physicians and Surgeons, Columbia University, New York, New York 10032.
Biochemistry (UNITED STATES) Jan 12, 1988, 27 (1) p108-15, ISSN 0006-2960 Journal Code: A0G
Contract/Grant No.: CA-46533, CA, NCI
Languages: ENGLISH
Document type: JOURNAL ARTICLE
High-resolution two-dimensional NMR studies have been completed on the self-**complementary** d(C-G-C-G-A-G-C-T-T-G-C-G) duplex (designated G.T 12-mer) and the self-**complementary** d(C-G-C-G-A-G-C-T-O4meT-G-C-G) duplex (designated G.O4meT 12-mer) containing G.T and G.O4meT pairs at identical positions four **base** pairs in from either end of the duplex. The exchangeable and nonexchangeable proton resonances have been assigned from an analysis of two-dimensional nuclear Overhauser enhancement (NOESY) spectra for the G.T 12-mer and G.O4meT 12-mer duplexes in H2O and D2O solution. The guanosine and thymidine imino protons in the G.T mismatch resonate at 10.57 and 11.98 ppm, respectively, and exhibit a strong NOE between themselves and to imino protons of flanking **base** pairs in the G.T 12-mer duplex. These results are consistent with wobble pairing at the G.T mismatch site involving two imino proton-carbonyl **hydrogen bonds** as reported previously [Hare, D. R., Shapiro, L., & Patel, D. J. (1986) Biochemistry 25, 7445-7456]. In contrast, the guanosine imino proton in the G.O4meT pair resonates at 8.67 ppm. The large upfield chemical shift of this proton relative to that of the imino proton resonance of G in the G.T mismatch or in G.C **base** pairs indicates that **hydrogen bonding** to O4meT is either very weak or absent. This guanosine imino proton has an NOE to the OCH3 group of O4meT across the pair and NOEs to the imino protons of flanking **base**

pairs.(ABSTRACT TRUNCATED AT 250 WORDS)

11/3,AB/34 (Item 34 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

05122736 88057375
Synthesis and structural studies by nuclear magnetic resonance of dodecadeoxynucleotides containing O6-methylguanine, O6-ethylguanine and O4-methylthymine.
Li BF; Swann PF; Kalnik M; Patel DJ
Courtauld Institute of Biochemistry, Middlesex Hospital Medical School, London, UK.
IARC scientific publications (FRANCE) 1987, (84) p44-8, ISSN 0300-5038 Journal Code: GKU
Languages: ENGLISH
Document type: JOURNAL ARTICLE
Self-**complementary** dodecadeoxynucleotides containing either one O6-methylguanine (O6-meGua), one O6-ethylguanine (O6-etGua) or one O4-methylthymine (O4-meT) have been synthesized. They form double-stranded DNA in solution. The structures of these DNA helices containing O6-meGua:cytosine (C), O6-meGua:thymine (T), O6-etGua:C and Gua:O4-meT **base** pairs have been investigated by nuclear magnetic resonance (NMR). All these **modified bases** stack into the helix with the normal anti-glycosidic torsion angle; only in the helix containing an O6-etGua:C **base** pair was there evidence of significant distortion of the DNA structure. NMR did not show a strong **hydrogen bond** between N1 of Gua and N3 of O4-meT in the Gua:O4-meT **base** pair, or between N1 of O6-meGua and N3 of T in the O6meGua:T **base** pair. This casts doubt on the previously accepted structures for O4-meT:Gua and O6-meGua:T mispairs.

11/3,AB/35 (Item 35 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

04896577 86187740
Structural studies of the O6meG.T interaction in the d(C-G-T-G-A-A-T-T-C-O6meG-C-G) duplex.
Patel DJ; Shapiro L; Kozlowski SA; Gaffney BL; Jones RA
Biochemistry (UNITED STATES) Mar 11 1986, 25 (5) p1036-42, ISSN 0006-2960 Journal Code: A0G
Contract/Grant No.: 1R01 GM34504, GM, NIGMS; GM31483, GM, NIGMS; SO7RR05359-23, RR, NCRR
Languages: ENGLISH
Document type: JOURNAL ARTICLE
High-resolution proton and phosphorus NMR studies are reported on the self-**complementary** d(C1-G2-T3-G4-A5-A6-T7-T8-C9-O6meG10-C11-G12) duplex (henceforth called O6meG.T 12-mer), which contains T3.O6meG10 interactions in the interior of the helix. The imino proton of T3 is observed at 9.0 ppm, exhibits a temperature-independent chemical shift in the premelting transition range, and broadens out at the same temperature as the imino proton of the adjacent G2.C11 toward the end of the helix at pH 6.8. We observed inter **base** pair nuclear Overhauser effects (NOEs) between the **base** protons at the T3.O6meG10 **modification** site and the protons of flanking G2.C11 and G4.C9 **base** pairs, indicative of the stacking of the T3 and O6meG10 **bases** into the helix. Two-dimensional correlated (COSY) and nuclear Overhauser effect (NOESY) studies have permitted assignment of the **base** and sugar H1', H2', and H2'' nonexchangeable protons in the O6meG.T 12-mer duplex. The observed NOEs demonstrate an anti conformation about all the glycosidic bonds, and their directionality supports formation of a right-handed helix in solution. The observed NOEs between the T3.O6meG10 interaction and the

adjacent G2.C[illegible] and G4.C9 **base** pairs at the **modification** site exhibit small departures from patterns for a [illegible]ular helix in the O6.meG.T 12-mer duplex. The phosphorus resonances exhibit a 0.5 ppm spectral dispersion indicative of an unperturbed phosphodiester backbone for the O6meG.T 12-mer duplex. We propose a model for pairing of T3 and O6meG10 at the **modification** site in the O6meG.T 12-mer duplex. (ABSTRACT TRUNCATED AT 250 WORDS)

11/3,AB/36 (Item 36 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

04896576 86187739
Structural studies of the O6meG.C interaction in the d(C-G-C-G-A-A-T-T-C-O6meG-C-G) duplex.
Patel DJ; Shapiro L; Kozlowski SA; Gaffney BL; Jones RA
Biochemistry (UNITED STATES) Mar 11, 1986, 25 (5) p1027-36, ISSN 0006-2960 Journal Code: A0G
Contract/Grant No.: 1RO1 GM34504, GM, NIGMS; GM 31483, GM, NIGMS; SO7RR05359-23, RR, NCRR
Languages: ENGLISH
Document type: JOURNAL ARTICLE
One- and two-dimensional nuclear magnetic resonance (NMR) experiments have been undertaken to investigate the conformation of the d(C1-G2-C3-G4-A5-A6-T7-T8-C9-O6meG10-C11-G12) self-**complementary** dode canucleotide (henceforth called O6meG.C 12-mer), which contains C3.O6meG10 interactions in the interior of the helix. We observe intact **base** pairs at G2.C11 and G4.C9 on either side of the **modification** site at low temperature though these **base** pairs are kinetically destabilized in the O6meG.C 12-mer duplex compared to the G.C 12-mer duplex. One-dimensional nuclear Overhauser effects (NOEs) on the exchangeable imino protons demonstrate that the C3 and O6meG10 **bases** are stacked into the helix and act as spacers between the flanking G2.C11 and G4.C9 **base** pairs. The nonexchangeable **base** and H1', H2', H2'', H3', and H4' protons have been completely assigned in the O6meG.C 12-mer duplex at 25 degrees C by two-dimensional correlated (COSY) and nuclear Overhauser effect (NOESY) experiments. The observed NOEs and their directionality demonstrate that the O6meG.C 12-mer is a right-handed helix in which the O6meG10 and C3 **bases** maintain their anti conformation about the glycosidic bond at the **modification** site. The NOEs between the H8 of O6meG10 and the sugar protons of O6meG10 and adjacent C9 exhibit an altered pattern indicative of a small conformational change from a regular duplex in the C9-O6meG10 step of the O6meG.C 12-mer duplex. We propose a pairing scheme for the C3.O6meG10 interaction at the **modification** site. Three phosphorus resonances are shifted to low field of the normal spectral dispersion in the O6meG.C 12-mer phosphorus spectrum at low temperature, indicative of an altered phosphodiester backbone at the **modification** site. These NMR results are compared with the corresponding parameters in the G.C 12-mer, which contains Watson-Crick **base** pairs at the same position in the helix.

11/3,AB/37 (Item 37 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

04770133 86104460
Covalent carcinogenic lesions in DNA: NMR studies of O6-methylguanosine containing oligonucleotide duplexes.
Patel DJ; Shapiro L; Kozlowski SA; Gaffney BL; Kuzmich S; Jones RA
Biochimie (FRANCE) Jul-Aug 1985, 67 (7-8) p861-86, ISSN 0300-9084 Journal Code: A14
Contract/Grant No.: 1RO1 GM34504, GM, NIGMS; GM31483, GM, NIGMS; SO7RR05359-23, RR, NCRR

Languages: ENGLISH
Document ty[redacted] JOURNAL ARTICLE

We report on proton and phosphorus high resolution NMR investigations of the self-**complementary** dodecanucleotide d(C1-G2-N3-G4-A5-A6-T7-T8-C9-O6meG10-C11-G12) duplexes (henceforth called O6 meG.N 12-mers), N = C, T, A and G, which contain N3.O6meG10 interactions in the interior of the helix. These sequences containing a single **modified** O6meG per strand were prepared by phosphoamidite synthesis and provide an excellent model for probing the structural basis for covalent carcinogenic lesions in DNA. Distance dependent nuclear Overhauser effect (NOE) measurements and line widths of imino protons demonstrate that the N3 and O6meG.10 **bases** stack into the duplex and are flanked by stable Watson-Crick **base** pairs at low temperature for all four O6meG.N 12-mer duplexes. The imino proton of T3 in the O6meG.T 12-mer and G3 in the O6meG.N 12-mer helix, which are associated with the **modification** site, resonate at unusually high field (8.5 to 9.0 ppm) compared to imino protons in Watson-Crick **base** pairs (12.5 to 14.5 ppm). The nonexchangeable **base** and sugar protons have been assigned from two dimensional correlated (COSY) and nuclear Overhauser effect (NOESY) measurements on the O6meG.N 12-mer helices. The directionality of the distance dependent NOEs establish all O6meG.N duplexes to be right-handed helices in solution. The glycosidic torsion angles are in the anti range at the N3.O6meG10 **modification** site except for O6meG10 in the O6meG.G 12-mer duplex which adopts a syn configuration. This results in altered NOEs between the G3 (anti).O6meG10 (syn) pair and flanking G2.C11 and G4.C9 **base** pairs in the O6meG.G 12-mer duplex. We observe pattern reversal for cross peaks in the COSY spectrum linking the sugar H1' protons with the H2',2" protons at the G2 and O6meG10 residues in the O6meG.N 12-mer duplexes with the effect least pronounced for the O6meG.T 12-mer helix. The proton chemical shift and NOE data have been analyzed to identify regions of conformational perturbations associated with N3.O6meG10 **modification** sites in the O6meG.N 12-mer duplexes. The proton decoupled phosphorus spectrum of O6meG.T 12-mer duplex exhibits an unperturbed phosphodiester backbone in contrast to the phosphorus spectra of the O6meG.C 12-mer, O6meG.G 12-mer and O6meG.A 12-mer duplexes which exhibit phosphorus resonances dispersed over 2 ppm characteristic of altered phosphodiester backbones at the **modification** site. Tentative proposals are put forward for N3.O6meG10 pairing models **based** on the available NMR data and serve as a guide for the design of future experiments.

11/3,AB/38 (Item 38 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

03920136 84005101
Theoretical NMR study of the pre-melting transition in the d-(CGCGAATTCGCG) and d-(CGCGTATACGCG) self-**complementary** duplexes.
Giessner-Prettre C; Pullman B
FEBS letters (NETHERLANDS) Mar 21 1983, 153 (2) p329-31, ISSN 0014-5793 Journal Code: EUH
Languages: ENGLISH
Document type: JOURNAL ARTICLE

The difference between their shielding in a B-DNA duplex and in the single strand having the same conformation has been calculated for all **base** protons of the dodecamers d-(CGCGAATTCGCG) and d-(CGCGTATACGCG). The calculated chemical shift variations reproduce the qualitative features of the shifts which occur during the pre-melting of the helices. This agreement shows that the pre-melting mechanism consists mainly of a lengthening of the **hydrogen bonds** between the two strands (in line opening) and that the conformation of the ribophosphate backbone and the orientation of the **bases** do not undergo major **modifications** during the first step of the melting.

11/3,AB/39 (Item 39 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
(c) format only 2000 Dialog Corporation. All rts. reserv.

03692345 81077277
Priming and inhibitory activities of RNAs for the influenza viral transcriptase do not require **base** pairing with the virion template RNA.
Krug RM; Broni BA; LaFiandra AJ; Morgan MA; Shatkin AJ
Proceedings of the National Academy of Sciences of the United States of America (UNITED STATES) Oct 1980, 77 (10) p5874-8, ISSN 0027-8424
Journal Code: PV3
Contract/Grant No.: CA 08748, CA, NCI; AI 11772, AI, NIAID
Languages: ENGLISH
Document type: JOURNAL ARTICLE
Capped ribopolymers lacking a sequence **complementary** to the common 3' end of the influenza virion RNA segments effectively stimulated transcription of these RNAs by the virion-associated transcriptase. Thus, stimulation of transcription results not from **hydrogen bonding** between the capped RNA and the 3' end of the virion RNA but presumably from a specific interaction of the capped RNA with protein(s) in the transcriptase complex. Although no specific nucleotide sequence was required for priming activity, capped mRNAs with diminished secondary structure were preferred as primers. Inosine-substituted or bisulfite-**modified** capped reovirus mRNAs were at least 3- to 5-fold more effective as primers than were the native capped mRNAs. On the other hand, inosine substitution or bisulfite treatment of the uncapped form of reovirus mRNAs converted them from essentially inactive species to potent inhibitors of the transcriptase reaction primed by either ApG or globin mRNA. These effects of reduced secondary structure also most probably reflect an interaction of the exogenous RNAs with transcriptase protein(s). The results obtained from screening a series of native uncapped ribopolymers were consistent with inhibitory activity requiring the absence of most **hydrogen bonding** in the ribopolymer and also suggested that specific structural feature(s) of the nucleotides in the chain were important.

11/3,AB/40 (Item 40 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
(c) format only 2000 Dialog Corporation. All rts. reserv.

02672149 80011655
Local destabilisation of a DNA double helix by a T--T wobble pair.
Cornelis AG; Haasnoot JH; den Hartog JF; de Rooij M; van Boom JH; Cornelis A
Nature (ENGLAND) Sep 20 1979, 281 (5728) p235-6, ISSN 0028-0836
Journal Code: NSC
Languages: ENGLISH
Document type: JOURNAL ARTICLE
Nuclear magnetic resonance is a technique which permits direct observation of the Waton--Click **hydrogen-bonded** ring imino protons (guanine N1H and thymine N3H). As the formation and disruption of **hydrogen bonds** of double-helical RNA and DNA structures are key events during various biological processes, NMR thus provides a useful tool for studying the fluctuational mobility of the individual **base** pairs. Indeed, several NMR studies of oligo- and polynucleotides have been carried out to probe the structure and dynamics of **nucleic acids** in solution (for a review see ref. 1). The present study constitutes the first part of our attempt to assess the influence of non-**complementary** **base** pairs on the stability of **nucleic acid** double helices. We report the spectral assignment and temperature-dependent NMR profiles of the **hydrogen-bonded** imino protons of the two DNA fragments shown in Fig. 1. The assignment is **based** solely on experimental grounds using the principle of chemical **modification**. It

will be demonstrated that the introduction of a non-**complementary** (wobble) **base** pair in a DNA duplex introduces an extra melting site in addition to the sequential melting which starts with the terminal **base** pairs in the double helix structure.

11/3,AB/41 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

12037005 BIOSIS NO.: 199900317524
An A-DNA structure with two independent duplexes in the asymmetric unit.
AUTHOR: Savitha G; Viswamitra M A(a)
AUTHOR ADDRESS: (a)Department of Physics, Indian Institute of Science, Bangalore, 560 012**India
1999
JOURNAL: Acta Crystallographica Section D Biological Crystallography 55 (6):p1136-1143 June, 1999
ISSN: 0907-4449
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English
SUMMARY LANGUAGE: English

ABSTRACT: The crystal and molecular structure of the self-**complementary** A-DNA decamer sequence d(G4CGC4) was solved at 1.9 ANG resolution. The decamer crystallizes in space group P21 with two independent duplexes in the asymmetric unit. Duplex 1 has interactions which are distributed symmetrically about its length compared with duplex 2. The two end **base** pairs of duplex 1 have a similar NHcntdotcntdotcntdotO **hydrogen-bond** pattern involving GGC segments of duplex 2 and a symmetry-related neighbour, while the end **base** pairs of duplex 2 interact with the GCC and GGG segments of its symmetry-related neighbours through NHcntdotcntdotcntdotO and NHcntdotcntdotcntdotN **hydrogen bonds** and a water-mediated **hydrogen bond** between the carboxyl groups of C40 and C8. In addition to the C4'-C5' torsion angle gamma assuming the trans conformation in certain steps, this angle also adopts the gauche- conformation at C37 as opposed to the preferred gauche+ conformation, with a concomitant change in phosphodiester P-O5' (alpha) in the opposite sense. This facilitates stacking between adjacent **bases**. The study suggests that the structural alterations in the two molecules in the asymmetric unit originate from an inherent propensity of the d(G4CGC4) **base** sequence for varied intermolecular interactions and malleability.

11/3,AB/42 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

07701019 BIOSIS NO.: 000092036800
MOLECULAR MECHANICAL STUDY OF STRUCTURAL-ENERGETICAL ASPECTS OF THE **COMPLEMENTARY** ADDRESSED **MODIFICATION** OF **NUCLEIC ACIDS** BY REACTIVE DERIVATIVES OF OLIGONUCLEOTIDES CARRYING A 3'-TERMINAL 4-N-2 CHLOROETHYL-N-METHYLAMINO-BENZYLIDENE GROUP
AUTHOR: VOROB'EV YU N
AUTHOR ADDRESS: NOVOSIB. INST. BIOORG. CHEM., SIB. DEP., ACAD. SCI. USSR, NOVOSIBIRSK 630090, USSR.
JOURNAL: BIOORG KHIM 17 (2). 1991. 211-222.
FULL JOURNAL NAME: Bioorganicheskaya Khimiya
CODEN: BIKHD
RECORD TYPE: Abstract
LANGUAGE: RUSSIAN

ABSTRACT: Cal[redacted]ations of probabilities of the **complementary** addressed **m[redacted]fication** of a target **nucleic a[redacted]** by derivatives of oligonucleotides carrying a 4-[N-(2-chloroethyl)-N-methyl]aminobenzylidene group attached to the 3'-end (3'-BDO) have been made. The results show that the **complementary** complex of a target NA with 3'-BDO having R-configuration of carbon atom of the dioxalane ring is more stable than the complex including the S-stereoisomer. The S- and R-epimeres of 3'-BDO have essentially different positional abilities for alkylation of the target. The R-epimer alkylates best of all the third **base** of the target NA from terminal **complementary** pair of the complex. The S-epimer has another site the most sensitive to alkylation, which is a terminal **complementary base** of the target NA or the adjacent nonpaired **base**. Formation of the alkylation complexes are accompanied with a loss or a breakdown of **hydrogen bonds** in the terminal **complementary base** pair, thus decreasing the efficiency of alkylation. The modelling results are considered along with experimental data on **modification** which therefore can be interpreted on the fundamental structural level.

11/3,AB/43 (Item 3 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

06800661 BIOSIS NO.: 000088110100
NMR AND COMPUTATIONAL CHARACTERIZATION OF THE N DEOXYGUANOSIN-8-YLAMINOFLUORENE ADDUCT AFG OPPOSITE ADENOSINE IN DNA AFG-SYN A-ANTI PAIR FORMATION AND ITS PH DEPENDENCE
AUTHOR: NORMAN D; ABUAF P; HINGERTY B E; LIVE D; GRUNBERGER D; BROYDE S; PATEL D J
AUTHOR ADDRESS: DEP. BIOCHEM. MOL. BIOPHYSICS, COLL. PHYSICIANS SURG., COLUMBIA UNIV., NEW YORK, N.Y. 10032, USA.
JOURNAL: BIOCHEMISTRY 28 (18). 1989. 7462-7476.
FULL JOURNAL NAME: Biochemistry
CODEN: BICHA
RECORD TYPE: Abstract
LANGUAGE: ENGLISH

ABSTRACT: This paper reports on a combined two-dimensional NMR and energy minimization computational characterizaton of the conformation of the N-(deoxyguanosyl-8-yl)aminofluorene adduct [(AF)G] positioned across adenosine in a DNA oligomer duplex as a function of pH in aqueous solution. This study was undertaken on the d[C1-C2-A3-T4-C5-_(_A_F_)_G_6-C7-T8-A9-C10-C11].cntdot.[G12-G13-T14-A15-G16-_A_1_7-G18-A19-T20-G21-G22] **complementary** undecamer [(AF)G 11-mer duplex]. The **modification** of the single G6 on the pyrimidine-rich strand was accomplished by reaction of the oligonucleotide with N-acetoxy-2-(acetylamino)fluorene and subsequent deacetylation under alkaline conditions. The HPLC-purified **modified** strand was annealed with the unmodified purine-rich strand to generate the (AF)G 11-mer duplex. The exchangeable and nonexchangeable protons are well resolved and narrow in the NMR spectra of the (AF)G 11-mer duplex so that the **base** and the majority of sugar **nucleic acid** protons, as well as several aminofluorene ring protons, have been assigned following analysis of two-dimensional NOESY and COSY data sets at pH 6.9, 30.degree. C in H2O and D2O solution. The NOE distance constraints establish that the glycosidic torsion angle is syn at (AF)G6 and anti at A17, which results in the aminofluorene ring being positioned in the minor groove. A very large downfield shift is detected at the H2' sugar proton of (AF)G6 associated with the (AF)G6[syn].cntdot.A17 [anti] alignment in the (AF)G 11-mer duplex. The NMR parameters demonstrate formation of Watson-Crick C5.cntdot.G18 and C7.cntdot.G16 **base** pairs on either side of the (AF)G6[syn].cntdot.A17[anti] **modification** site with the imino proton of G18 more stable to

exchange th[redacted] the imino proton of G16. Several nonexchangeable aminofluore[redacted] protons undergo large downfiel[redacted] shifts as do the imino and H8 protons of G16 on lowering of the pH from neutrality to acidic values for the (AF)G 11-mer duplex. Both the neutral and acidic pH conformations have been defined by assigning the NOE constraints in the [C5-(AF)G6-C7].cntdot.[G16-A17-G18] segment centered about the **modification** site and incorporating them in distance constrained minimized potential energy calculations in torsion angle space with the DUPLEX program. A series of NOEs between the aminofluorene protons and the DNA sugar protons in the neutral pH conformation establish that the aminofluorene ring spans the minor groove and is directed toward the G16-A17-G18 sugar-phosphate backbone on the partner strands. An unconstrained minimum energy neutral pH conformation for the (AF)G 11-mer duplex was generated from the minimization runs which satisfies the NMR distance constraints and is stabilized by hydrophobic interactions between the aminofluorene ring and the walls of the minor groove. The backbone of A17 adopts a BII conformation (.epsilon., .zeta. = g-, t) and the sugar ring of G16 adopts a C3'-endo pucker which facilitates, in part, a small displacement of A17 toward the major groove and minimizes the total solvent exposure of aminofluorene and A17 at the **modification** site. There is poor stacking between **bases** in the C5-(AF)G6-C7 segment but strong stacking between **bases** in the G16-A17-G18 segment consistent with the large upfield shifts of the H8 protons of G16 and G18 in the (AF)G 11-mer duplex. The NOE constraints establish that the (AF)G6[syn].cntdot.A17[anti] alignment is retained on lowering of the pH but is accompanied by the loss of contacts between the aminofluorene ring of (AF)G6 and the G16-A17-G18 sugar-phosphate backbone on the partner strand. A minimum energy acidic pH conformation is proposed for the [C5-_(_A_F_)_G_6-C7].cntdot.[G16-_A_1_7-G18] segment involving protonated (AF)G6[syn].cntdot.A17[anti]pairing stabilized by one **hydrogen bond** between the N1 of protonated A17 and the O6 of (AF)G6. This alignment results in the displacement of the aminofluorene ring away from the helix axis in the minor groove. Our studies establish an interplay between hydrophobic and **hydrogen-bonding** contributions to the stabilization of the

```
=> s 2 aminodeoxyadenosine
L1          13 2 AMINODEOXYADENOSINE
=> s 2 thiodeoxythymidine
L2           2 2 THIODEOXYTHYMIDINE
=> s deoxyinosine
L3         767 DEOXYINOSINE
=> s deoxypyrrolopyrimidine
L4           0 DEOXYPYRROLOPYRIMIDINE
=> s 2 thiodeoxycytidine
L5           0 2 THIODEOXYCYTIDINE
=> s deoxyguanosine
L6        6752 DEOXYGUANOSINE
=> s deoxycytidine
L7        5903 DEOXYCYTIDINE
=> s deoxyadenosine
L8        6466 DEOXYADENOSINE
=> s deoxythymidine
L9        4513 DEOXYTHYMIDINE
=> s l3 or l6 or l7 or l8 or l9
L10      20535 L3 OR L6 OR L7 OR L8 OR L9
=> s l10 and 5 triphosphate
L11       1022 L10 AND 5 TRIPHOSPHATE
=> s s11 and nucleotid?
L12        150 S11 AND NUCLEOTID?
=> rd
```

Should have been L11 !!

```
RD IS NOT A RECOGNIZED COMMAND
The previous command name entered was not recognized by the system.
For a list of commands available to you in the current file, enter
"HELP COMMANDS" at an arrow prompt (=>).

=> dr

DR IS NOT A RECOGNIZED COMMAND
```

SEARCH STEPS. For more information, enter HELP SEARCH STEPS at an arrow prompt.

With fields for which a thesaurus file exists, search queries may be enriched with additional search terms such as Narrower Terms, Broader Terms, Related Terms, etc. For more information about using a thesaurus in searches, enter HELP THESAURUS at an arrow prompt in the desired file.

When SmartSelect L-numbers are searched, a new SmartSelect L-number can be created that contains those terms for which there were no postings. For more information, enter HELP SET AUDIT at an arrow prompt.

=> dup rem

ENTER L# LIST OR (END):

ENTER L# LIST OR (END):end

=> dup rem l12

PROCESSING COMPLETED FOR L12
L13 122 DUP REM L12 (28 DUPLICATES REMOVED)

=> dup rem l1

PROCESSING COMPLETED FOR L1
L14 11 DUP REM L1 (2 DUPLICATES REMOVED)

=> dup rem l2

PROCESSING COMPLETED FOR L2
L15 2 DUP REM L2 (0 DUPLICATES REMOVED)

=> display l15

ENTER ANSWER NUMBER OR RANGE (1):1-2

ENTER DISPLAY FORMAT (BIB):bib abs

L15 ANSWER 1 OF 2 CAPLUS COPYRIGHT 2000 ACS
AN 1970:415154 CAPLUS
DN 73:15154
TI Synthesis of 2,4-dithiothymine nucleosides
AU Faerber, Peter; Scheit, Karl H.
CS Abt. Chem., Max-Planck-Inst. Exp. Med., Goettingen, Ger.
SO Chem. Ber. (1970), 103(5), 1307-11
CODEN: CHBEAM
DT Journal
LA German
AB Reaction of 2',3',5'-tri-O-benzoyl-4-thio-5-methyluridine with P2S5 and K2S in Tetralin gave 55% 2,4-dithio-5-methyluridine. **2-Thiodeoxythymidine** was prepd. in 95% yield from 3'-O-acetyl-O2,5'-anhydrodeoxythymidine, Et3N, and H2S at -70.degree. via 3'-O-acetyl-**2-thiodeoxythymidine**, which on refluxing with P2S5 gave 60% 2,4-dithiodeoxythymidine.

L15 ANSWER 2 OF 2 CAPLUS COPYRIGHT 2000 ACS
AN 1970:431551 CAPLUS
DN 73:31551
TI Synthesis and characterization of a copolymer consisting of alternating deoxyadenosine- and **2-thiodeoxythymidine** nucleotides

AU Lezius, [redacted] G.
CS Abt. Che[redacted] Max Planck Inst. Exp. Med., G[redacted]ttingen, Ger.
SO Eur. J. Biochem. (1970), 14(1), 154-60
CODEN: EJBCAI
DT Journal
LA English
AB Starting from **2-thiodeoxythymidine** (I), the mono- and triphosphates of the nucleoside analog were prepd. by enzymic phosphorylation with thymidine kinase and thymidylate kinase, resp. I triphosphate was also obtained by chem. pyrophosphorylation of the monophosphate. I triphosphate is a substrate for Escherichia coli DNA polymerase. A copolymer consisting of alternating dA and I nucleotides is
synthesized extensively by the enzyme. The polymer was characterized by nearest neighbor anal., sedimentation and buoyant d. in the anal. ultracentrifuge, uv spectra, and stability against thermal and alk. denaturation.

=> display l13 1-122 bib abs

L13 ANSWER 1 OF 122 SCISEARCH COPYRIGHT 2000 ISI (R) DUPLICATE 1
AN 2000:577790 SCISEARCH
GA The Genuine Article (R) Number: 337DZ
TI Sequence and molecular analysis of the rpoA cluster genes from Xanthomonas
campestris pv. campestris
AU Lai J Y; Huang C F; Tseng Y H; Yang M T (Reprint)
CS NATL CHUNGHSING UNIV, INST MOL BIOL, TAICHUNG 402, TAIWAN (Reprint); NATL CHUNGHSING UNIV, INST MOL BIOL, TAICHUNG 402, TAIWAN
CYA TAIWAN
SO BIOCHIMICA ET BIOPHYSICA ACTA-GENE STRUCTURE AND EXPRESSION, (24 JUL 2000)
Vol. 1492, No. 2-3, pp. 553-559.
Publisher: ELSEVIER SCIENCE BV, PO BOX 211, 1000 AE AMSTERDAM, NETHERLANDS.
ISSN: 0167-4781.
DT Article; Journal
FS LIFE
LA English
REC Reference Count: 27
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS
AB The Xanthomonas campestris rpsM (S13)-rpsK (**S11**)-rpsD (S4)-rpoA (alpha)-rplQ (L17) cluster, encoding RNA polymerase alpha-subunit and four ribosomal proteins, reside in a 3164-bp DNA region.
The N-terminal sequence of the authentic alpha-protein determined chemically matches that predicted from the **nucleotide** sequence. rplQ is monocistronic, instead of being co-transcribed with the other genes as in Escherichia coli. Antiserum against the His-tagged alpha-protein cross-reacted with the E. coli alpha-protein. (C) 2000 Elsevier Science B.V. All rights reserved.

L13 ANSWER 2 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 2000:353958 CAPLUS
TI The mitochondrial DNA of Dictyostelium discoideum: complete sequence, gene
content and genome organization
AU Ogawa, S.; Yoshino, R.; Angata, K.; Iwamoto, M.; Pi, M.; Kuroe, K.; Matsuo, K.; Morio, T.; Urushihara, H.; Yanagisawa, K.; Tanaka, Y.
CS Institute of Biological Sciences, University of Tsukuba, Tsukuba, 305-8572, Japan
SO Mol. Gen. Genet. (2000), 263(3), 514-519
CODEN: MGGEAE; ISSN: 0026-8925

PB Springer-Verlag
DT Journal
LA English
AB We present an overview of the gene content and organization of the mitochondrial genome of Dictyostelium discoideum. The mitochondria genome consists of 55,564 bp with an A + T content of 72.6%. The identified genes include those for two rRNAs (rnl and rns), 18 tRNAs, ten subunits of the NADH dehydrogenase complex (nad1, 2, 3, 4, 4L, 5, 6, 7, 9 and 11), apocytochrome b (cytb), three subunits of the cytochrome oxidase (cox1/2 and 3), four subunits of the ATP synthase complex (atp1, 6, 8 and 9), 15 ribosomal proteins, and five other ORFs, excluding intronic ORFs. Notable features of D. discoideum mtDNA include the following. (1) All genes are encoded on the same strand of the DNA and a universal genetic code is used. (2) The cox1 gene has no termination codon and is fused to the downstream cox2 gene. The 13 genes for ribosomal proteins and four ORF genes form a cluster 15.4 kb long with several gene overlaps. (3) The no. of tRNAs encoded in the genome is not sufficient to support the synthesis of mitochondrial protein. (4) In total, five group I introns reside in rnl and cox1/2, and three of those in cox1/2 contain four free-standing ORFs. We compare the genome to other sequenced mitochondrial genomes, particularly that of Acanthamoeba castellanii.
RE.CNT 39
RE
(1) Angata, K; Curr Genet 1995, V27, P249 CAPLUS
(2) Angata, K; Gene 1995, V153, P49 CAPLUS
(3) Attardi, G; Annu Rev Cell Biol 1988, V4, P289 CAPLUS
(4) Baldauf, S; Proc Natl Acad Sci USA 1997, V94, P12007 CAPLUS
(5) Burger, G; J Mol Biol 1995, V245, P522 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L13 ANSWER 3 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 2000:462 CAPLUS
DN 132:217810
TI Characterization of the Leptospira interrogans S10-spc-.alpha. operon
AU Zuerner, R. L.; Hartskeerl, R. A.; van de Kemp, H.; Bal, A. E.
CS Agricultural Research Service, National Animal Disease Center, Zoonotic Diseases Research Unit, U.S. Department of Agriculture, Ames, IA, 50010, USA
SO FEMS Microbiol. Lett. (2000), 182(2), 303-308
CODEN: FMLED7; ISSN: 0378-1097
PB Elsevier Science B.V.
DT Journal
LA English
AB A ribosomal protein gene cluster from the spirochaete Leptospira interrogans was characterized. This locus is homologous to the Escherichia coli S10, spc, and .alpha. operons. Anal. of L. interrogans RNA showed that the ribosomal protein genes within this cluster are co-transcribed, thus forming an operon. Two transcription initiation sites were mapped by primer extension upstream of fus, the first gene in this cluster, and sequences from this region provided promoter activity in E. coli. Transcription terminates near a predicted stem-loop structure following rplQ, the last gene in the cluster. These data suggest that 2 promoters upstream of fus direct transcription of this 17.5-kb ribosomal protein gene cluster. Comparison of the L. interrogans S10-spc-.alpha. cluster to homologous loci from Borrelia burgdorferi and Treponema pallidum provided evidence that this region of the genome underwent several rearrangements during spirochaete evolution.
RE.CNT 20
RE
(1) Ballard, S; Gene 1998, V216, P21 CAPLUS

(2) Ballard, [redacted] Mol Microbiol 1993, V8, P739 CAPLUS
(4) Brosius, [redacted] Gene 1984, V27, P151 CAPLUS
(5) Cerretti, D; Nucleic Acids Res 1983, V11, P2599 CAPLUS
(6) Chomczynski, P; Anal Biochem 1987, V162, P156 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L13 ANSWER 4 OF 122 SCISEARCH COPYRIGHT 2000 ISI (R) DUPLICATE 2
AN 2000:503225 SCISEARCH
GA The Genuine Article (R) Number: 328VD
TI Sequence analysis of Pns11, a nonstructural protein of rice gall dwarf virus, and its expression and detection in infected rice plants and vector insects
AU Moriyasu Y; Ishikawa K; Kikuchi A; Imanishi S; Tomita S; Akutsu K; Omura T
(Reprint)
CS NATL AGR RES CTR, TSUKUBA, IBARAKI 3058666, JAPAN (Reprint); NATL AGR RES CTR, TSUKUBA, IBARAKI 3058666, JAPAN; NATL INST SERICULTURAL & ENTOMOL SCI, TSUKUBA, IBARAKI 3058634, JAPAN; IBARAKI UNIV, FAC AGR, IBARAKI, OSAKA 3000332, JAPAN
CYA JAPAN
SO VIRUS GENES, (MAY 2000) Vol. 20, No. 3, pp. 237-241.
Publisher: KLUWER ACADEMIC PUBL, SPUIBOULEVARD 50, PO BOX 17, 3300 AA DORDRECHT, NETHERLANDS.
ISSN: 0920-8569.
DT Article; Journal
FS LIFE
LA English
REC Reference Count: 19
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS
AB The **nucleotide** sequence of genome segment **S11** of rice gall dwarf virus (RGDV), a member of Phytoreovirus, was determined. The segment encodes a putative protein of 40 kDa that exhibits approximately 37% homology at the amino acid level to the nonstructural proteins Pns10 of rice dwarf and wound tumor viruses, which are other members of Phytoreovirus. A band of a protein with an apparent molecular mass of 40 kDa was specifically detected in an analysis of cells transfected with **S11** cDNA. An antiserum raised against this protein reacted with a protein of approximately 40 kDa after fractionation by SDS-PAGE of materials prepared from infected plants and from viruliferous vector insects. However, the antiserum did not react with purified viral proteins. These results suggest that **S11** encodes a nonstructural protein of RGDV. This protein was named Pns11.

L13 ANSWER 5 OF 122 SCISEARCH COPYRIGHT 2000 ISI (R)
AN 2000:540623 SCISEARCH
GA The Genuine Article (R) Number: 333YE
TI Gene conversion of ribosomal DNA in Nicotiana tabacum is associated with undermethylated, decondensed and probably active gene units
AU Lim K Y; Kovarik A; Matyasek R; Bezdek M; Lichtenstein C P; Leitch A R
(Reprint)
CS UNIV LONDON QUEEN MARY & WESTFIELD COLL, SCH BIOL SCI, MILE END RD, LONDON E1 4NS, ENGLAND (Reprint); UNIV LONDON QUEEN MARY & WESTFIELD COLL, SCH BIOL SCI, LONDON E1 4NS, ENGLAND; ACAD SCI CZECH REPUBL, INST BIOPHYS, CS-61265 BRNO, CZECH REPUBLIC
CYA ENGLAND; CZECH REPUBLIC
SO CHROMOSOMA, (JUL 2000) Vol. 109, No. 3, pp. 161-172.
Publisher: SPRINGER VERLAG, 175 FIFTH AVE, NEW YORK, NY 10010.
ISSN: 0009-5915.
DT Article; Journal
FS LIFE
LA English
REC Reference Count: 44

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB We examined the structure, intranuclear distribution and activity of ribosomal DNA (rDNA) in Nicotiana sylvestris (2n=2x=24) and N. tomentosiformis (2n=2x=24) and compared these with patterns in N. tabacum (tobacco, 2n=4x=48). We also examined a long-established N. tabacum culture, TBY-2. Nicotiana tabacum is an allotetraploid thought to be derived from ancestors of N. sylvestris (S-genome donor) and N. tomentosiformis (T-genome donor). Nicotiana sylvestris has three rDNA loci, one locus each on chromosomes 10, 11, and 12. In root-tip meristematic interphase cells, the site on chromosome 12 remains condensed and inactive, while the sires on chromosomes 10 and 11 show activity at the proximal end of the locus only. Nicotiana tomentosiformis has one major locus on chromosome 3 showing activity and a minor, inactive locus on chromosome II. In N. tabacum cv. 095-55, there are four rDNA loci on T3, S10, **S11**/t and S12 (**S11**/t carries a small T-genome translocation). The locus on S12 remains condensed and inactive in root-tip meristematic cells while the others show activity, including decondensation at interphase and secondary constrictions at metaphase. Nicotiana tabacum DNA digested with methylcytosine-sensitive enzymes revealed a hybridisation pattern for rDNA that resembled that of N. tomentosiformis and not N. sylvestris. The data indicate that active, undermethylated genes are of the N. tomentosiformis type. Since S-genome chromosomes of N. tabacum show rDNA expression, the result indicates rDNA gene conversion of the active rDNA units on these chromosomes. Gene conversion in N. tabacum is consistent with the results of previous work. However, using primers specific for the S-genome rDNA intergenic sequences (IGS) in the polymerase chain reaction (PCR) show that rDNA gene conversion has not gone to completion in N. tabacum. Furthermore, using methylation-insensitive restriction enzymes we demonstrate that about 8% of the rDNA units remain of the N. sylvestris type (from ca. 75% based on the sum of the rDNA copy numbers in the parents). Since the active genes are likely to be of an N. tomentosiformis type, the N. sylvestris type units are presumably contained within inactive loci (i.e. on chromosome S12). Nicotiana sylvestris has approximately three times as much rDNA as the other two species, resulting in much condensed rDNA at interphase. This species also has three classes of IGS, indicating gene conversion has not homogenised repeat length in this species. The results suggest that methylation and/or DNA condensation has reduced or prevented gene conversion from occurring at inactive genes at rDNA loci. Alternatively, active undermethylated units may be vulnerable to gene conversion, perhaps because they are decondensed and located in close proximity within the nucleolus at interphase. In TBY-2, restriction enzymes showed hybridisation patterns that were similar to, but different from, those of N. tabacum. In addition, TBY-2 has elevated rDNA copy number and variable numbers of rDNA loci, all indicating rDNA evolution in culture.

L13 ANSWER 6 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1999:593400 CAPLUS
DN 131:347279
TI The complete chloroplast DNA sequence of the green alga Nephroselmis olivacea: insights into the architecture of ancestral chloroplast genomes
AU Turmel, Monique; Otis, Christian; Lemieux, Claude
CS Canadian Institute for Advanced Research, Program in Evolutionary Biology and Departement de Biochimie, Universite Laval, Quebec, PQ, G1K 7P4, Can.
SO Proc. Natl. Acad. Sci. U. S. A. (1999), 96(18), 10248-10253
CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
AB Green plants seem to form two sister lineages: Chlorophyta, comprising the

green algal classes Prasinophyceae, Ulvophyceae, Trebouxiophyceae, and Chlorophyceae, and Streptophyta, comprising the Charophyceae and land plants. We have detd. the complete chloroplast DNA (cpDNA) sequence (200,799 bp) of Nephroselmis olivacea, a member of the class (Prasinophyceae) thought to include descendants of the earliest-diverging green algae. The 127 genes identified in this genome represent the largest gene repertoire among the green algal and land plant cpDNAs completely sequenced to date. Of the Nephroselmis genes, 2 (ycf81, and ftsI, a gene involved in peptidoglycan synthesis) have not been identified in any previously investigated cpDNA; 5 genes [ftsW, rnE, ycf62, rnpB, and trnS(cga)] have been found only in cpDNAs of nongreen algae; and 10 others (ndh genes) have been described only in land plant cpDNAs. Nephroselmis and land plant cpDNAs share the same quadripartite structure-which is characterized by the presence of a large rRNA-encoding inverted repeat and two unequal single-copy regions-and very similar sets of genes in corresponding genomic regions. Given that our phylogenetic analyses place Nephroselmis within the Chlorophyta, these structural characteristics were most likely present in the cpDNA of the common ancestor of chlorophytes and streptophytes. Comparative analyses of chloroplast genomes indicate that the typical quadripartite architecture and gene-partitioning pattern of land plant cpDNAs are ancient features that may have been derived from the genome of the cyanobacterial progenitor of chloroplasts. Our phylogenetic data also offer insight into the chlorophyte ancestor of euglenophyte chloroplasts.

RE.CNT 35
RE
(2) Bhattacharya, D; Plant Physiol 1998, V116, P9 CAPLUS
(3) Boudreau, E; Plant Mol Biol 1994, V24, P585 CAPLUS
(4) Burrows, P; EMBO J 1998, V17, P868 CAPLUS
(5) Chapman, R; Molecular Systematics of Plant II DNA Sequencing 1998, P508 CAPLUS
(6) Donachie, W; Annu Rev Microbiol 1993, V47, P199 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L13 ANSWER 7 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1999:307009 CAPLUS
DN 131:142865
TI Vascular endothelial genes that are responsive to tumor necrosis factor-.alpha. in vitro are expressed in atherosclerotic lesions, including inhibitor of apoptosis protein-1, stannin, and two novel genes
AU Horrevoets, Anton J. G.; Fontijn, Ruud D.; Van Zonneveld, Anton Jan; De Vries, Carlie J. M.; Cate, Jan Wouter ten; Pannekoek, Hans
CS Department of Biochemistry and Vascular Medicine of the Academic Medical Center, University of Amsterdam, Amsterdam, 1105 AZ, Neth.
SO Blood (1999), 93(10), 3418-3431
CODEN: BLOOAW; ISSN: 0006-4971
PB W. B. Saunders Co.
DT Journal
LA English
AB Activation and dysfunction of endothelial cells play a prominent role in patho-physiol. processes such as atherosclerosis. The identification by differential display of 106 cytokine-responsive gene fragments from endothelial cells, activated by monocyte conditioned medium or tumor necrosis factor-.alpha., are described. A minority of the fragments (22/106) represent known genes involved in various processes, including leukocyte trafficking, vesicular transport, cell cycle control, apoptosis, and cellular protection against oxidative stress. Full-length cDNA clones

were obtained for five novel transcripts that were induced or repressed >10-fold in vitro. These novel human cDNAs CA2_1, CG12_1, GG10_2, AG8_1, and GG2_1 encoded inhibitor of apoptosis protein-1 (hIAP-1), homologs of apolipoprotein-L, mouse rabkinesin-6, rat stannin, and a novel 188 amino acid protein, resp. Expression of 4 novel transcripts was shown by in situ hybridization on healthy and atherosclerotic vascular tissue, using monocyte chemotactic protein-1 as a marker for inflammation. CA2-1 (hIAP-1) and AG8-1 were expressed by endothelial cells and macrophage foam cells of the inflamed vascular wall. CG12_1 (apolipoprotein-L like) was specifically expressed in endothelial cells lining the normal and atherosclerotic iliac artery and aorta. These results substantiate the complex change in the gene expression pattern of vascular endothelial cells, which accompanies the inflammatory reaction of atherosclerotic lesions.

RE.CNT 48
RE
(2) Balla, G; J Biol Chem 1992, V267, P18148 CAPLUS
(3) Bauer, D; Nucleic Acids Res 1993, V21, P4272 CAPLUS
(4) Brand, K; J Clin Invest 1996, V97, P1715 CAPLUS
(5) Chu, Z; Proc Natl Acad Sci USA 1997, V94, P10057 CAPLUS
(6) Cines, D; Blood 1998, V91, P3527 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L13 ANSWER 8 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1999:662200 CAPLUS
DN 132:9537
TI The complete mitochondrial DNA sequences of Nephroselmis olivacea and Pedinomonas minor: two radically different evolutionary patterns within green algae
AU Turmel, Monique; Lemieux, Claude; Burger, Gertraud; Lang, B. Franz; Otis, Christian; Plante, Isabelle; Gray, Michael W.
CS Program in Evolutionary Biology, Canadian Institute for Advanced Research, Quebec, PQ, G1K 7P4, Can.
SO Plant Cell (1999), 11(9), 1717-1729
CODEN: PLCEEW; ISSN: 1040-4651
PB American Society of Plant Physiologists
DT Journal
LA English
AB Green plants appear to comprise two sister lineages, Chlorophyta (classes Chlorophyceae, Ulvophyceae, Trebouxiophyceae, and Prasinophyceae) and Streptophyta (Charophyceae and Embryophyta, or land plants). To gain insight into the nature of the ancestral green plant mitochondrial genome, we have sequenced the mitochondrial DNAs (mtDNAs) of Nephroselmis olivacea and Pedinomonas minor. These two green algae are presumptive members of the Prasinophyceae. This class is thought to include descendants of the earliest diverging green algae. We find that Nephroselmis and Pedinomonas mtDNAs differ markedly in size, gene content, and gene organization. Of the green algal mtDNAs sequenced so far, that of Nephroselmis (45,223 bp) is the most ancestral (minimally diverged) and occupies the phylogenetically most basal position within the Chlorophyta. Its repertoire of 69 genes closely resembles that in the mtDNA of Prototheca wickerhamii, a later diverging trebouxiophycean green alga. Three of the Nephroselmis genes (nad10, rpl14, and rnpB) have not been identified in previously sequenced mtDNAs of green algae and land plants. In contrast, the 25,137-bp Pedinomonas mtDNA contains only 22 genes and retains few recognizably ancestral features. In several respects, including gene content and rate of sequence divergence, Pedinomonas mtDNA resembles the reduced mtDNAs of chlamydomonad algae, with which it is robustly affiliated in phylogenetic analyses. Our results confirm the existence of

two radically different patterns of mitochondrial genome evolution within the green algae.
RE.CNT 25
RE
(1) Lonergan, K; J Mol Biol 1994, V239, P476 CAPLUS
(2) Ma, D; Plant Mol Biol 1992, V18, P1001 CAPLUS
(3) Martin, N; Nucleic Acids Symp Ser 1997, V36, P42 CAPLUS
(4) McCracken, D; New Phytol 1980, V86, P39 CAPLUS
(8) Oda, K; J Mol Biol 1992, V223, P1 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L13 ANSWER 9 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1999:662197 CAPLUS
DN 132:31513
TI Complete sequence of the mitochondrial DNA of the red alga Porphyra purpurea: cyanobacterial introns and shared ancestry of red and green algae
AU Burger, Gertraud; Saint-Louis, Diane; Gray, Michael W.; Lang, B. Franz
CS Program in Evolutionary Biology, Canadian Institute for Advanced Research,
Toronto, ON, M5G 1Z8, Can.
SO Plant Cell (1999), 11(9), 1675-1694
CODEN: PLCEEW; ISSN: 1040-4651
PB American Society of Plant Physiologists
DT Journal
LA English
AB The mitochondrial DNA (mtDNA) of Porphyra purpurea, a circular-mapping genome of 36,753 bp, has been completely sequenced. A total of 57 densely
packed genes has been identified, including the basic set typically found in animals and fungi, as well as seven genes characteristic of protist and
plant mtDNAs and specifying ribosomal proteins and subunits of succinate:ubiquinone oxidoreductase. The mitochondrial large subunit rRNA
gene contains two group II introns that are extraordinarily similar to those found in the cyanobacterium Calothrix sp, suggesting a recent lateral intron transfer between a bacterial and a mitochondrial genome. Notable features of P. purpurea mtDNA include the presence of two 291-bp inverted repeats that likely mediate homologous recombination, resulting in genome rearrangement, and of numerous sequence polymorphisms in the coding and intergenic regions. Comparative anal. of red algal mitochondrial genomes from five different, evolutionarily distant orders reveals that rhodophyte mtDNAs are unusually uniform in size and gene order. Finally, phylogenetic analyses provide strong evidence that red algae share a common ancestry with green algae and plants.
RE.CNT 133
RE
(1) Altschul, S; J Mol Biol 1990, V215, P403 CAPLUS
(2) Anderson, S; Nature 1981, V290, P457 CAPLUS
(3) Andersson, S; Nature 1998, V396, P133 CAPLUS
(4) Beagley, C; Genetics 1998, V148, P1091 CAPLUS
(5) Bhattacharya, D; Mol Biol Evol 1993, V10, P689 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L13 ANSWER 10 OF 122 SCISEARCH COPYRIGHT 2000 ISI (R)
AN 1999:472350 SCISEARCH
GA The Genuine Article (R) Number: 205YW
TI Efficient reconstitution of functional Escherichia coli 30S ribosomal subunits from a complete set of recombinant small subunit ribosomal proteins
AU Culver G M; Noller H F (Reprint)
CS UNIV CALIF SANTA CRUZ, SINSHEIMER LABS, CTR MOL BIOL RNA, SANTA CRUZ, CA 95064 (Reprint); UNIV CALIF SANTA CRUZ, SINSHEIMER LABS, CTR MOL BIOL RNA,

SANTA CR[redacted] CA 95064
CYA USA
SO RNA-A PUBLICATION OF THE RNA SOCIETY, (JUN 1999) Vol. 5, No. 6, pp. 832-843.
Publisher: CAMBRIDGE UNIV PRESS, 40 WEST 20TH STREET, NEW YORK, NY 10011-4211.
ISSN: 1355-8382.
DT Article; Journal
FS LIFE
LA English
REC Reference Count: 40
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB Previous Studies have shown that the 30S ribosomal subunit of Escherichia coli can be reconstituted in vitro from individually purified ribosomal proteins and 16S ribosomal RNA, which were isolated from natural 30S subunits. We have developed a 30S subunit reconstitution system that uses only recombinant ribosomal protein components. The genes encoding E. coli ribosomal proteins S2-S21 were cloned, and all twenty of the individual proteins were overexpressed and purified. Reconstitution, following standard procedures, using the complete set of recombinant proteins and purified 16S ribosomal RNA is highly inefficient. Efficient reconstitution of 30S subunits using these components requires sequential addition of proteins, following either the 30S subunit assembly map (Mizushima & Noura, 1970, Nature 226:1214-1218; Held et al., 1974, J Biol Chem 249:3103-3111) or following the order of protein assembly predicted from in vitro assembly kinetics (Powers et al., 1993; J Mol Biol 232:362-374)In the first procedure, the proteins were divided into three groups, Group I (S4, S7, S8, S15, S17, and S20), Group II (S5, S6, S9, **S11**, S12, S13, S16, S18, and S19), and Group III (S2, S3, S10, S14, and S21), which were sequentially added to 16S rRNA with a 20 min incubation at 42 degrees C following the addition of each group. In the second procedure; the proteins were divided into Group I (S4, S6, **S11**, S15, S16, S17, S18, and S20), Group 11:(S7, S8, S9, S13, and S19), Group II' (S5 and S12) and Group III (S2, S3, S10, S14, and S21). Similarly efficient reconstitution is observed whether the proteins are grouped according to the assembly map or according to the results of in vitro 30S subunit assembly kinetics.

Although reconstitution of 30S subunits using the recombinant proteins is slightly less efficient than reconstitution using a mixture of total proteins isolated from 30S subunits, it is much more efficient than reconstitution using proteins that were individually isolated from ribosomes. Particles reconstituted from the recombinant proteins sediment at 30S in sucrose gradients, bind tRNA in a template-dependent manner, and associate with 50S subunits to form 70S ribosomes that are active in poly(U)-directed polyphenylalanine synthesis. Both the protein composition and the dimethyl sulfate modification pattern of 16S ribosomal RNA are similar for 30S subunits reconstituted with either recombinant proteins or proteins isolated as a mixture from ribosomal subunits as well as for natural 30S subunits.

L13 ANSWER 11 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1999:214683 CAPLUS
DN 131:1330
TI Structure of two maize phytase genes and their spatio-temporal expression during seedling development
AU Maugenest, Sebastien; Martinez, Isabelle; Godin, Beatrice; Perez, Pascual; Lescure, Anne-Marie
CS Laboratoire de Biologie des Semences, INRA INA-PG, Versailles, 78026, Fr.
SO Plant Mol. Biol. (1999), 39(3), 503-514.
CODEN: PMBIDB; ISSN: 0167-4412

PB Kluwer Academic Publishers
DT Journal
LA English
AB Up to 80% of Zea mays L. grain phosphorus is stored in the form of phytin in the embryo. Our objective is to det. the control of phytin mobilization during germination and seedling growth. A maize phytase cDNA, phy **S11**, has been previously characterized (Maugenest et al., Biochem J 322: 511-517, 1997). In the present work, phy **S11** was used to screen a maize genomic library and two distinct genes, PHYT I and PHYT II, were isolated and sequenced. The transcribed sequences of these two genes presented a strong homol. whereas the untranscribed upstream and downstream sequences appeared very different. Northern blot anal. and in situ hybridization showed a high accumulation of phytase mRNA at the early steps of germination in the coleorhiza, radicle cortex and coleoptile parenchyma. Phytase expression was also detected at a lower extent in the scutellum. In adult plants, northern blot analyses revealed low but significant levels of phytase mRNA in the roots. In situ hybridizations on root cross-sections localized phytase mRNA in rhizodermis, endodermis and pericycle layers. Immunolocalization anal. showed phytase accumulation at the same sites as its mRNA. A RT-PCR approach was used in an attempt to discriminate between the transcripts from each gene in the different situations. These expts. indicate that both genes are expressed during germination, whereas only PHYT I is expressed in adult roots. This suggests that signals responsible for phytase gene expression in roots are different from those responsible for gene expression during germination.
RE.CNT 23
RE
(2) Bohnert, H; Plant Cell 1995, V7, P1099 CAPLUS
(3) Frohman, M; Proc Natl Acad Sci USA 1988, V85, P8998 CAPLUS
(6) Hanley, B; Nucl Acids Res 1988, V16, P7159 CAPLUS
(8) Hooley, R; Plant Mol Biol 1994, V26, P1529 CAPLUS
(11) Laboure, A; Biochem J 1993, V295, P413 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L13 ANSWER 12 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1999:169388 CAPLUS
DN 131:28495
TI Sequence analysis of a 32-kb region including the major ribosomal protein gene clusters from alkaliphilic Bacillus sp. strain C-125
AU Takami, Hideto; Takaki, Yoshihiro; Nakasone, Kaoru; Hirama, Chie; Inoue, Akira; Horikoshi, Koki
CS Deep-sea Microorganisms Research Group, Japan Marine Science and Technology Center, Kanagawa, 237-0061, Japan
SO Biosci., Biotechnol., Biochem. (1999), 63(2), 452-455
CODEN: BBBIEJ; ISSN: 0916-8451
PB Japan Society for Bioscience, Biotechnology, and Agrochemistry
DT Journal
LA English
AB Forty-one open reading frames (ORFs) were identified in a 32-kb DNA fragment of alkaliphilic Bacillus sp. C-125. A similarity search using the BSORF database found 37 ORFs with significant sequence similarity to B. subtilis RNA polymerase subunits, elongation factor G, elongation factor Tu, and ribosomal proteins. Each ORF product showed more than 70% identity to those of B. subtilis. Gene organization in the region of str, S10, spc, and the .alpha. cluster was highly conserved among three strains, C-125, B. subtilis, and B. stearothermophilus.
RE.CNT 4
RE
(1) Herfurth, E; FEBS Lett 1994, V351, P114 CAPLUS
(2) Kimura, J; FEBS Lett 1987, V210, P85 CAPLUS
(3) Ramakrishnan, V; J Biol Chem 1991, V266, P880 CAPLUS

(4) Triglia, T; Nucleic Acid Res 1988, V16, P8186 CAPLUS

L13 ANSWER 13 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1999:744245 CAPLUS
DN 132:118133
TI Gene organization and sequence of the region containing the ribosomal protein genes RPL13A and RPS11 in the human genome and conserved features in the mouse genome
AU Higa, S.; Yoshihama, M.; Tanaka, T.; Kenmochi, N.
CS School of Medicine, Department of Biochemistry, University of the Ryukyus, Okinawa, Japan
SO Gene (1999), 240(2), 371-377
CODEN: GENED6; ISSN: 0378-1119
PB Elsevier Science B.V.
DT Journal
LA English
AB We have detd. the organization and sequence of the region contg. two ribosomal protein (rp) genes in the human and mouse genomes. The two genes, human RPL13A and RPS11, and mouse Rpl13a and Rps11, are tandemly located in both genomes with an interval of only 4.6 kb in the case of the human genes and 1.6 kb in the case of the mouse genes. The human RPL13A and RPS11 are 4236 bp and 3254 bp in length and comprise eight and five exons resp., whereas the mouse Rps11 is 1951 bp long and has five exons. Structural comparison of these genes, including previously reported mouse Rpl13a, revealed a significant conservation of sequences in the promoter regions. Although most rp genes are dispersed throughout the human genome, the conserved features and adjacent localization indicate possible coordinate transcription of the two genes. Furthermore, we have found that four small nucleolar RNA (snoRNA) genes are located in the introns of the two rp genes, both human and mouse. U32, U33, and U34 snoRNAs are encoded in introns 2, 4, and 5 of RPL13A resp., and U35 in the sixth intron of RPL13A and the third intron of RPS11. The same organization of these snoRNA genes was also obsd. in the case of the mouse genes.
RE.CNT 34
RE
(1) Antoine, M; Biochem J 1998, V336, P327 CAPLUS
(2) Ashworth, L; Nat Genet 1995, V11, P422 CAPLUS
(4) Cherry, J; Nucleic Acids Res 1998, V26, P73 CAPLUS
(5) Dudov, K; Cell 1984, V37, P457 CAPLUS
(6) Gilley, J; DNA Cell Biol 1998, V17, P591 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L13 ANSWER 14 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1999:722035 CAPLUS
DN 132:74333
TI Complete structure of the chloroplast genome of Arabidopsis thaliana
AU Sato, Shusei; Nakamura, Yasukazu; Kaneko, Takakazu; Asamizu, Erika; Tabata, Satoshi
CS Kazusa DNA Research Institute, Chiba, 292-0812, Japan
SO DNA Res. (1999), 6(5), 283-290
CODEN: DARSE8; ISSN: 1340-2838
PB Universal Academy Press
DT Journal
LA English
AB The complete **nucleotide** sequence of the chloroplast genome of Arabidopsis thaliana has been detd. The genome as a circular DNA composed of 154,478 bp contg. a pair of inverted repeats of 26,264 bp, which are sepd. by small and large single copy regions of 17,780 bp and 84,170 bp, resp. A total of 87 potential protein-coding genes including 8 genes duplicated in the inverted repeat regions, 4 rRNA genes and 37 tRNA genes

(30 gene species) representing 20 amino acid species were assigned to the genome on basis of similarity to the chloroplast genes previously reported for other species. The translated amino acid sequences from resp. potential protein-coding genes showed 63.9% to 100% sequence similarity to those of the corresponding genes in the chloroplast genome of Nicotiana tabacum, indicating the occurrence of significant diversity in the chloroplast genes between two dicot plants. The sequence data and gene information are available on the World Wide Web database KAOS (Kazusa Arabidopsis data Opening Site) at http://www.kazusa.or.jp/arabi/.

RE.CNT 30
RE
(1) Altschul, S; J Mol Biol 1990, V215, P403 CAPLUS
(3) Douglas, S; J Mol Evol 1999, V48, P236 CAPLUS
(4) Hallick, R; Nucleic Acid Res 1993, V21, P3537 CAPLUS
(6) Kaiser, J; Science 1996, V274, P30 CAPLUS
(7) Kaneko, T; DNA Res 1996, V3, P109 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L13 ANSWER 15 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1999:168958 CAPLUS
DN 131:28494
TI Cloning of the RNA polymerase .alpha. subunit gene from Thermus thermophilus HB8 and characterization of the protein
AU Wada, Takashi; Yamazaki, Toshio; Kuramitsu, Seiki; Kyogoku, Yoshimasa
CS Institute for Protein Research, Osaka University, Suita, 565-0871, Japan
SO J. Biochem. (Tokyo) (1999), 125(1), 143-150
CODEN: JOBIAO; ISSN: 0021-924X
PB Japanese Biochemical Society
DT Journal
LA English
AB The region contg. the RNA polymerase alpha. subunit (RNAP.alpha.) gene (rpoA) and the ribosomal protein genes of a thermophilic eubacterial strain, Thermus thermophilus (Tt) HB8, was cloned from a genomic DNA library by Southern hybridization. The gene order in this region is rpl36-rps13-rps11-rps4-rpoA-rpl17, which is identical to that in some other eubacteria. The rpoA gene encodes a 315 amino acid residue protein with a mol. wt. of 35,013, the amino acid sequence showing 42% identity to that of Escherichia coli. (Ec). From the results of comparison of the amino acid sequence and the predicted secondary structure of the C-terminal domain of Tt RNAP.alpha. (Tt .alpha.CTD) with those of Ec, the overall folding is expected to be similar. However, amino acid residues Asn268 and Cys269 in Ec .alpha.CTD, which are essential for its interaction with DNA or regulatory proteins, were replaced by His and Ser, resp., in Tt .alpha.CTD. By means of a T7-based expression system in Ec cells, Tt RNAP.alpha. was overexpressed and purified. The high thermostability of Tt RNAP.alpha. was demonstrated by the CD spectra.

RE.CNT 44
RE
(1) Bedwell, D; Nucleic Acids Res 1985, V13, P3891 CAPLUS
(2) Boylan, S; J Bacteriol 1989, V171, P2553 CAPLUS
(3) Carbonetti, N; J Bacteriol 1994, V176, P7267 CAPLUS
(4) Cho, E; Nucleic Acids Res 1996, V24, P4565 CAPLUS
(5) Choy, H; EMBO J 1995, V14, P4523 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L13 ANSWER 16 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1999:262852 CAPLUS
DN 131:70348
TI Identification, molecular cloning, and characterization of subunit 11 of the human 26S proteasome
AU Hoffman, Laura; Gorbea, Carlos; Rechsteiner, Martin
CS School of Medicine, Department of Biochemistry, University of Utah, Salt

Lake City, UT, USA
SO FEBS Lett. (1999), 449(1), 88-92
CODEN: FEBLAL; ISSN: 0014-5793
PB Elsevier Science B.V.
DT Journal
LA English
AB We sequenced five peptides from subunit 11 (**S11**), a 43 kDa protein of the human 26S proteasome, and used this information to clone its cDNA. The **S11** cDNA encodes a 376 amino acid protein with a pI of 5.6 and a mol. mass of 42.9 kDa. Translation of **S11** RNA in the presence of [35S]methionine produces a radiolabeled protein that co-migrates with **S11** of the human 26S proteasome on SDS-PAGE. Polyclonal antiserum made against recombinant **S11** recognizes a protein of the same size in exts. of bacteria expressing **S11** and in purified 26S proteasomes from human red blood cells or rabbit reticulocytes. The **S11** sequence does not contain motifs that suggest a biol. function. **S11** is, however, the human homolog of Rpn9, a recently identified subunit of the yeast 26S proteasome.

RE.CNT 24
RE
(1) Andre, B; Biochem Biophys Res Commun 1994, V205, P1201 CAPLUS
(2) Baumeister, W; Cell 1998, V92, P367 CAPLUS
(3) Confalonieri, F; BioEssays 1995, V17, P639 CAPLUS
(4) Coux, O; Annu Rev Biochem 1996, V65, P801 CAPLUS
(5) Deveraux, Q; J Biol Chem 1994, V269, P7059 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L13 ANSWER 17 OF 122 SCISEARCH COPYRIGHT 2000 ISI (R)DUPLICATE 3
AN 1999:798657 SCISEARCH
GA The Genuine Article (R) Number: 246FJ
TI Cloning, sequencing, and characterization of ribosomal protein and RNA polymerase genes from the region analogous to the alpha-operon of Escherichia coli in halophilic archaea, Halobacterium halobium
AU Sano K; Taguchi A; Furumoto H; Uda T; Itoh T (Reprint)
CS HIROSHIMA PREFECTURAL UNIV, SCH BIORESOURCES, SHOBARA, HIROSHIMA 72700, JAPAN (Reprint); HIROSHIMA PREFECTURAL UNIV, SCH BIORESOURCES, SHOBARA, HIROSHIMA 72700, JAPAN
CYA JAPAN
SO BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (14 OCT 1999) Vol. 264, No. 1, pp. 24-28.
Publisher: ACADEMIC PRESS INC, 525 B ST, STE 1900, SAN DIEGO, CA 92101-4495.
ISSN: 0006-291X.
DT Article; Journal
FS LIFE
LA English
REC Reference Count: 21
ABSTRACT IS AVAILABLE IN THE ALL AND LALL FORMATS
AB A determination was made of the **nucleotide** sequence of the 3215-bp region of a ribosomal protein gene cluster (HS13, HS4, HS11, and HeL18), RNA polymerase (RNA poly D), and tRNA genes (tRNAser and tRNAarg) of halophilic Archaea Halobacterium halobium, which is analogous to the alpha-operon of Escherichia coli (tRNAser-HS13-HS4-HS11-RNA poly D-tRNAarg-HeL18). The seven-gene string was preceded by a pseudoknot-like structure similar to the proposed S4 ribosomal protein binding site of the alpha-operon mRNA leader in E. coli. Using an inducible expression system H. halobium HS4 was produced in large amounts in E. coli, and immunoblot analysis showed the S4 to constitute a 21-kDa polypeptide component of the ribosome. Analysis of the deduced amino acids sequence revealed that the HS13, HS4, and HS11 sequences including the RNA polymerase subunit are more similar to their eukaryotic than to their bacterial counterparts. HeL18, located downstream of the gene cluster analogous to the E. coli alpha-operon (S13-**S11**-S4-RNA poly D-L17), was similar to both

the eukaryotic (eL18) and eubacterial ribosomal protein L15 located in the spc-operon, but not to L17 positioned as the terminal gene of-the bacterial alpha-operon, Academic Press.

L13 ANSWER 18 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1998:728569 CAPLUS
DN 130:3062
TI Granulocytic Ehrlichia antigens and cDNAs and methods for diagnosis and vaccination
IN Murphy, Cheryl A.; Storey, James; Beltz, Gerald A.; Coughlin, Richard T.
PA Aquila Biopharmaceuticals, Inc., USA
SO PCT Int. Appl., 154 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9849313	A2	19981105	WO 1998-US8265	19980424
	WO 9849313	A3	19990114		
	W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
	CA 2258277	AA	19981105	CA 1998-2258277	19980424
	AU 9872563	A1	19981124	AU 1998-72563	19980424
	EP 915980	A2	19990519	EP 1998-919870	19980424
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
PRAI	US 1997-44933		19970425		
	WO 1998-US8265		19980424		

AB The present invention relates, in general, to granulocytic Ehrlichia (GE) proteins. In particular, the present invention relates to nucleic acid mols. coding for GE S2, S7, S22, S23, C6.1, C6.2, **S11**, E8, E46#1, and E46#2 proteins; purified GE S2, S7, S22, S23, C6.1, C6.2, **S11**, E8, E46#1, and E46#2 proteins and polypeptides; recombinant nucleic acid mols.; cells contg. the recombinant nucleic acid mols.; antibodies having binding affinity specifically to GE S2, S7, S22, S23, C6.1, C6.2, **S11**, E8, E46#1, and E46#2 proteins and polypeptides; hybridomas contg. the antibodies; nucleic acid probes for the detection of nucleic acids encoding GE S2, S7, S22, S23, C6.1, C6.2, **S11**, E8, E46#1, and E46#2 proteins; a method of detecting nucleic acids encoding GE S2, S7, S22, S23, C6.1, C6.2, **S11**, E8, E46#1, and E46#2 proteins or polypeptides in a sample; kits contg. nucleic acid probes or antibodies; bioassays using the nucleic acid sequence, protein or antibodies of this invention to diagnose, assess, or prognose a mammal afflicted with ehrlichiosis; therapeutic uses, specifically vaccines comprising S2, S7, S22, S23, C6.1, C6.2, **S11**, E8, E46#1, and E46#2 proteins or polypeptides or nucleic acids; and methods of preventing or inhibiting ehrlichiosis in an animal.

L13 ANSWER 19 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1998:112461 CAPLUS
DN 128:189199
TI Plant phytases and nucleic acids encoding them, transgenic plants expressing phytase nucleic acids, and food or feed produced from such plants

IN Maugenest, Sebastien; Lescure, Anne-Marie; Perez, Pascual
PA Biocem, Fr; Institut National de la Recherche Agronomique; Maugenest, Sebastien; Lescure, Anne-Marie; Perez, Pascual
SO PCT Int. Appl., 101 pp.
CODEN: PIXXD2
DT Patent
LA French
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 9805785	A1	19980212	WO 1997-FR1443	19970801
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
FR 2751987	A1	19980206	FR 1996-9734	19960801
FR 2751987	B1	19981231		
CA 2261913	AA	19980212	CA 1997-2261913	19970801
AU 9739446	A1	19980225	AU 1997-39446	19970801
EP 938568	A1	19990901	EP 1997-936730	19970801
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				

PRAI FR 1996-9734 19960801
WO 1997-FR1443 19970801

AB The invention concerns plant phytases, in particular maize phytases, the genome DNA and cDNA sequences, as well as the transgenic plants or plant organs obtained from these sequences. Corn PHYT I and PHYT II genes as well as cDNA for the PHYT I gene were cloned and sequenced. Phytase gene expression during corn germination was analyzed by Northern blotting. The PHYT I gene cDNA was expressed in E. coli. The PHYT I and PHYT II genes were mapped to chromosome 3. The PHYT I gene promoter was controlled expression of phytase in embryonic organs while the PHYT II gene promoter was involved in control of mineral homeostasis in root cells.

L13 ANSWER 20 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1998:352026 CAPLUS
DN 129:91407
TI Cloning of gene using polynucleotide probes specifying targeting signals and DNA sequence of rice cytochrome oxidase complex subunit Vb gene
IN Kadowaki, Koichi
PA Norin Suisansho Nogyo Seibutsu Shigen Kenkyusho, Japan
SO Jpn. Kokai Tokkyo Koho, 13 pp.
CODEN: JKXXAF
DT Patent
LA Japanese
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI JP 10146200	A2	19980602	JP 1996-305365	19961115

AB Genes encoding proteins which are localized in specific organelles are cloned by hybridization with polynucleotide probes having sequences encoding targeting signals. The probes may be .gtoreq.15-**nucleotide**-length sequences contained in the given 2 sequences. A gene was cloned from the rice nuclear genome by plaque hybridization using a XhoI-NotI fragment of rice **s11**-2 gene, which encodes a targeting signal of a mitochondrial ribosomal protein **S11**, as a probe and identified as the coxVb gene encoding cytochrome oxidase complex Vb subunit. A **nucleotide** sequence complementary to coxVb gene

is useful for controlling expression of COXVb protein. The amino acid sequences of cytochrome oxidase complex Vb subunit and the target signal of ribosomal protein **S11** are presented.

L13 ANSWER 21 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1998:799091 CAPLUS
DN 130:149407
TI Structure and organization of the mitochondrial genome of the unicellular red alga Cyanidioschyzon merolae deduced from the complete **nucleotide** sequence
AU Ohta, Niji; Sato, Naoki; Kuroiwa, Tsuneyoshi
CS School of Human Science, Waseda University, Saitama, 359-1164, Japan
SO Nucleic Acids Res. (1998), 26(22), 5190-5198
CODEN: NARHAD; ISSN: 0305-1048
PB Oxford University Press
DT Journal
LA English
AB The complete **nucleotide** sequence of the mitochondrial genome of a very primitive unicellular red alga, Cyanidioschyzon merolae, has been detd. The mitochondrial genome of C. merolae contains 34 genes for proteins including unidentified open reading frames (ORFs) (three subunits of cytochrome c oxidase, apocytochrome b protein, three subunits of F1F0-ATPase, seven subunits of NADH ubiquinone oxidoreductase, three subunits of succinate dehydrogenase, four proteins implicated in c-type cytochrome biogenesis, 11 ribosomal subunits and two unidentified open reading frames), three genes for rRNAs and 25 genes for tRNAs. The G+C content of this mitochondrial genome is 27.2%. The genes are encoded on both strands. The genome size is comparatively small for a plant mitochondrial genome (32,211 bp). The mitochondrial genome resembles those of plants in its gene content because it contains several ribosomal protein genes and ORFs shared by other plant mitochondrial genomes. In contrast, it resembles those of animals in the genome organization, because it has very short intergenic regions and no introns. The gene set in this mitochondrial genome is a subset of that of Reclinomonas americana, an amoeboid protozoan. The results suggest that plant mitochondria originate from the same ancestor as other mitochondria and that most genes were lost from the mitochondrial genome at a fairly early stage of the evolution of the plants.
RE.CNT 32
RE
(2) Anderson, S; Nature 1981, V290, P457 CAPLUS
(3) Boer, P; Curr Genet 1991, V19, P309 CAPLUS
(4) Burger, G; J Mol Biol 1995, V245, P522 CAPLUS
(5) Denovan-Wright, E; Plant Mol Biol 1998, V36, P285 CAPLUS
(6) Felsenstein, J; J Mol Evol 1981, V17, P368 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L13 ANSWER 22 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1998:663483 CAPLUS
DN 130:12289
TI A new genetic locus in Sinorhizobium meliloti is involved in stachydrine utilization
AU Phillips, Donald A.; Sande, Eve S.; Vriezen, J. A. C.; De Bruijn, Frans J.; Le Rudulier, Daniel; Joseph, Cecillia M.
CS Department of Agronomy and Range Science, University of California, Davis, CA, 95616, USA
SO Appl. Environ. Microbiol. (1998), 64(10), 3954-3960
CODEN: AEMIDF; ISSN: 0099-2240
PB American Society for Microbiology
DT Journal
LA English
AB Stachydrine, a betaine released by germinating alfalfa seeds, functions as

an inducer of nodulation genes, a catabolite, and an osmoprotectant in Sinorhizobium meliloti. Two stachydrine-inducible genes were found in S. meliloti 1021 by mutation with a Tn5-luxAB promoter probe. Both mutant strains (S10 and **S11**) formed effective alfalfa root nodules, but neither grew on stachydrine as the sole carbon and nitrogen source. When grown in the absence or presence of salt stress, S10 and **S11** took up [14C]stachydrine as well as wild-type cells did, but neither used stachydrine effectively as an osmoprotectant. In the absence of salt stress, both S10 and **S11** took up less [14C]proline than wild-type cells did. S10 and **S11** appeared to colonize alfalfa roots normally in single-strain tests, but when mixed with the wild-type strain, their rhizosphere counts were reduced more than 50% (P .ltoreq. 0.01) relative to the wild type. These results suggest that stachydrine catabolism contributes to root colonization. DNA sequence anal. identified the mutated locus in **S11** as putA, and the luxAB fusion in that gene was induced by proline as well as stachydrine. DNA that restored the capacity of mutant S10 to catabolize stachydrine contained a new open reading frame, stcD. All data are consistent with the concept that stcD codes for an enzyme that produces proline by demethylation of N-methylproline, a degrdn. product of stachydrine.

RE.CNT 48
RE
(1) Altschul, S; J Mol Biol 1990, V215, P403 CAPLUS
(2) Backman, K; Proc Natl Acad Sci USA 1981, V78, P3743 CAPLUS
(4) Beringer, J; J Gen Microbiol 1974, V84, P188 CAPLUS
(6) de Bruijn, F; J Bacteriol 1989, V171, P1673 CAPLUS
(9) Ditta, G; Proc Natl Acad Sci USA 1980, V77, P7347 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L13 ANSWER 23 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1998:518495 CAPLUS
DN 129:255774
TI Cytoplasmic ribosomal protein genes of the fission yeast Schizosaccharomyces pombe display a unique promoter type: a suggestion for nomenclature of cytoplasmic ribosomal proteins in databases
AU Gross, Thomas; Kaufer, Norbert F.
CS Institut fur Genetik-Biozentrum, Technical University of Braunschweig, Braunschweig, 38106, Germany
SO Nucleic Acids Res. (1998), 26(14), 3319-3322
CODEN: NARHAD; ISSN: 0305-1048
PB Oxford University Press
DT Journal
LA English
AB We identified 34 new ribosomal protein genes in the Schizosaccharomyces pombe database at the Sanger Center coding for 30 different ribosomal proteins. All contain the Homol D-box in their promoter. We have shown that Homol D is, in this promoter type, the TATA-analog. Many promoters contain the Homol E-box, which serves as a proximal activation sequence. Furthermore, comparative sequence anal. revealed a ribosomal protein gene encoding a protein which is the equiv. of the mammalian ribosomal protein L28. The budding yeast Saccharomyces cerevisiae has no L28 equiv. Over the past 10 yr we have isolated and characterized nine ribosomal protein (rp) genes from the fission yeast S.pombe. This endeavor yielded promoters which we have used to investigate the regulation of rp genes. Since eukaryotic ribosomal proteins are remarkably conserved and several rp genes of the budding yeast S.cerevisiae were sequenced in 1985, we probed DNA fragments encoding S.cerevisiae ribosomal proteins with genomic libraries of S.pombe. The deduced amino acid sequence of the different isolated rp genes of fission yeast share between 65 and 85% identical amino acids with their counterparts of budding yeast.

L13 ANSWER 24 OF 122 SCISEARCH COPYRIGHT 2000 ISI (R)DUPLICATE 4
AN 1998:137432 SCISEARCH

GA The Genuine Article (R) Number: YV928
TI In vitro assembly of a ribonucleoprotein particle corresponding to the platform domain of the 30S ribosomal subunit
AU Agalarov S C; Zheleznyakova E N; Selivanova O M; Zheleznaya L A; Matvienko N I; Vasiliev V D; Spirin A S (Reprint)
CS RUSSIAN ACAD SCI, INST PROT RES, PUSHCHINO 142292, MOSCOW REGION, RUSSIA (Reprint); RUSSIAN ACAD SCI, INST PROT RES, PUSHCHINO 142292, MOSCOW REGION, RUSSIA; RUSSIAN ACAD SCI, INST THEORET & EXPT BIOPHYS, PUSHCHINO 142292, MOSCOW REGION, RUSSIA
CYA RUSSIA
SO PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (3 FEB 1998) Vol. 95, No. 3, pp. 999-1003.
Publisher: NATL ACAD SCIENCES, 2101 CONSTITUTION AVE NW, WASHINGTON, DC 20418.
ISSN: 0027-8424.
DT Article; Journal
FS LIFE
LA English
REC Reference Count: 26
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS
AB A fragment of the 16S RNA of Thermus thermophilus corresponding to the central domain (**nucleotides** 547-895) has been prepared by transcription in vitro. Incubation of this fragment with the total 30S ribosomal proteins has resulted in the formation of a compact 12S ribonucleoprotein particle, This particle contained five T. thermophilus proteins corresponding to Escherichia coli ribosomal proteins S6, S8, **S11**, S15, and possibly Sis, all of which were previously shown to interact with the central domain of the 16S RNA and to be localized in the platform (side bulge) of the 30S ribosomal subunit, When examined by electron microscopy, isolated particles have an appearance that is similar in size and shape to the corresponding morphological features of the 30S subunit, We conclude that the central domain of the 16S RNA can independently and specifically assemble with a defined subset of ribosomal proteins into a compact ribonucleoprotein particle corresponding to the platform (side bulge) of the 30S subunit.

L13 ANSWER 25 OF 122 SCISEARCH COPYRIGHT 2000 ISI (R)
AN 1999:37609 SCISEARCH
GA The Genuine Article (R) Number: 152CA
TI A screen for mutations that prevent lethality caused by expression of activated sevenless and Ras1 in the Drosophila embryo
AU Maixner A; Hecker T P; Phan Q N; Wassarman D A (Reprint)
CS NICHHD, CELL BIOL & METAB BRANCH, NIH, BLDG 18T, ROOM 101, BETHESDA, MD 20892 (Reprint); NICHHD, CELL BIOL & METAB BRANCH, NIH, BETHESDA, MD 20892
CYA USA
SO DEVELOPMENTAL GENETICS, (23 DEC 1998) Vol. 23, No. 4, pp. 347-361.
Publisher: WILEY-LISS, DIV JOHN WILEY & SONS INC, 605 THIRD AVE, NEW YORK, NY 10158-0012.
ISSN: 0192-253X.
DT Article; Journal
FS LIFE
LA English
REC Reference Count: 78
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS
AB Ras1 plays a critical role in receptor tyrosine kinase (RTK) signal transduction pathways that function during Drosophila development. We demonstrate that mis-expression of constitutively active forms of Ras1 (Ras1(V12)) and the Sevenless (Sev) RTK (Sev(**S11**)) during embryogenesis causes lethality due to inappropriate activation of RTK/Ras1

signaling pathways. Genetic and molecular data indicate that the rate of Sev(**S11**)/sev Ras1(V12) lethality is sensitive to the expression level of both transgenes. To identify genes that encode components of RTK/Ras1 signaling pathways or modulators of RNA polymerase II transcription, we took advantage of the dose-sensitivity of the system and screened for second site mutations that would dominantly suppress the lethality. The collection of identified suppressors includes the PR55 subunit of Protein Phosphatase 2A indicating that downstream of Sev and Ras 1 this subunit acts as a negative regulator of phosphatase activity. The isolation of mutations in the histone deacetylase RPD3 suggests that it functions as positive regulator of sev enhancer-driven transcription. Finally, the isolation of mutations in the Trithorax group gene devenir and the characterized allelism with the Breathless RTK encoding gene provides evidence for Ras1-mediated regulation of homeotic genes. Dev. Genet. 23:347-361, 1998. (C) 1998 Wiley-Liss, Inc.dagger

L13 ANSWER 26 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1998:451104 CAPLUS
DN 129:212252
TI Functional genomic analysis of rice dwarf virus
AU Li, Yi; Xu, Hong; Cheng, Mingfi; Zheng, Honghong; Mao, Zhijun; Xiao, Jin; Zhang, Fujian; Ming, Xiaotian; Qu, Lin; Liu, Yifei; Li, Wei; Zhao, Xiaolan; Pan, Naisui; Chen, Zhangliang
CS National Laboratory of Protein Engineering and Plant Genetic Engineering, College of Life Sciences, College of Life Sciences, Peking University, Beijing, 100871, Peop. Rep. China
SO Beijing Daxue Xuebao, Ziran Kexueban (1998), 34(2-3), 332-341
CODEN: PCTHAP; ISSN: 0479-8023
PB Beijing Daxue Chubanshe
DT Journal
LA Chinese
AB The rice dwarf virus full genome 12 gene segments were cloned and 25,000 **nucleotides** were sequenced. The gene functions of each segment were analyzed according to amino acid sequences and exptl. data. The coding regions of segments S6, S9, S10 and **S11** encoding nonstructural proteins were cloned into expression vector pTricHisA, pBV221, pTricHisB, pBV221, resp. The expressed products were analyzed by SDS-PAGE and further confirmed by Western-blotting. Using the E. coli expression products, the function of Pns11 was studied. Pns11 is a ds-/ss-RNA and DNA binding protein and it may play very important roles in virus genome assortment or packaging. Gene segments S2, S7, S8 and S9 which encode virus most outer coat protein, minor core protein, outer coat protein and nonstructural protein were transferred into rice via biolistic bombardment and regenerated rice plants were obtained.

L13 ANSWER 27 OF 122 SCISEARCH COPYRIGHT 2000 ISI (R)
AN 1998:116321 SCISEARCH
GA The Genuine Article (R) Number: YU698
TI Rice dwarf phytoreovirus segment **S11** encodes a nucleic acid binding protein
AU Xu H; Li Y (Reprint); Mao Z J; Li Y Y; Wu Z J; Qu L; An C C; Ming X T; Schiemann J; Casper R; Chen Z L
CS BEIJING UNIV, COLL LIFE SCI, NATL LAB PROT ENGN & PLANT GENET ENGN, BEIJING 100871, PEOPLES R CHINA (Reprint); BEIJING UNIV, COLL LIFE SCI, NATL LAB PROT ENGN & PLANT GENET ENGN, BEIJING 100871, PEOPLES R CHINA; DE MONTFORT UNIV, LEICESTER LE1 9BH, LEICS, ENGLAND; FED BIOL RES CTR AGR & FORESTRY BBA, INST BIOCHEM & PLANT VIROL, D-38104 BRAUNSCHWEIG, GERMANY
CYA PEOPLES R CHINA; ENGLAND; GERMANY
SO VIROLOGY, (20 JAN 1998) Vol. 240, No. 2, pp. 267-272.
Publisher: ACADEMIC PRESS INC JNL-COMP SUBSCRIPTIONS, 525 B ST, STE 1900,

SAN DIEGO, CA 92101-4495.
ISSN: 004[redacted]822.
DT Article; Journal
FS LIFE
LA English
REC Reference Count: 32
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB The function of rice dwarf virus segment 11 and the corresponding segments of other phytoreoviruses is not yet determined. The amino acid sequence of Pns11, encoded by segment 11, contains a putative zinc finger and five flanking basic regions at the C-terminus. The full-length Pns11 protein and three truncated derivatives, which lack the N-terminus, the zinc-finger, or the C-terminal five basic regions were expressed in Escherichia coil and their nucleic acid binding properties were studied. Pns11 interacts with single-and double-stranded forms of DNA and RNA in a sequence-nonspecific manner. The truncated derivative which contains both the zinc-finger and the C-terminal basic regions has the same binding properties as the full-length Pns11. However, removal of either of these domains prevents binding activity. The binding activity of Pns11 was drastically reduced when the blots were treated with a high concentration of EDTA. Moreover, Pns11 extracted from infected rice also binds to single-stranded RNA. These data suggest that RDV Pns11 binding activity is structure-dependent and it may play an important role in virus replication and/or genome assortment. (C) 1998 Academic Press.

L13 ANSWER 28 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1998:700488 CAPLUS
DN 130:35951
TI Transcriptional activities in the pituitaries of channel catfish before and after induced ovulation by injection of carp pituitary extract as revealed by expressed sequence tag analysis
AU Karsi, A.; Li, P.; Dunham, R. A.; Liu, Z. J.
CS Department of Fisheries and Allied Aquacultures, Auburn University, Auburn, AL, 36849, USA
SO J. Mol. Endocrinol. (1998), 21(2), 121-129
CODEN: JMLEEI; ISSN: 0952-5041
PB Society for Endocrinology
DT Journal
LA English

AB Expressed sequence tag (EST) anal. was adopted to address physiol. changes after injection of carp pituitary ext. for induction of ovulation. ESTs were analyzed from cDNA libraries constructed from mRNA isolated from channel catfish (Ictalurus punctatus) pituitaries before and after induction of ovulation by injection of carp pituitary ext. One hundred randomly picked clones were analyzed. Of the sequences generated, a large percentage (59%) of ESTs were identified as known genes by identity comparisons. These 59 clones of known gene products represent transcriptional products of 30 genes. The 41 clones of unknown gene products represent 33 genes. Expression of gonadotropin (GtH) .alpha.-subunit (149%) and prolactin (176%) was slightly enhanced as a result of induced ovulation. Large increases in frequencies of several peptide hormones were obsd. as a result of induced ovulation: GtH .beta.-I, 486%; GtH .beta.-II, 933%; growth hormone, 393%; proopiomelanocortin (POMC), 345%. POMC represented .apprx.21% of all transcriptional activity in the pituitaries after induced ovulation. This is the 1st study addressing physiol. changes after injection of carp pituitary ext., a procedure widely used in catfish hatcheries.

RE.CNT 51
RE
(1) Adams, M; Science 1991, V252, P1651 CAPLUS

(2) Aliyeva, E; Gene 1996, V180, P221 CAPLUS
(3) Artini, P; Journal of Endocrinological Investigation 1996, V19, P763 CAPLUS
(4) Azam, A; Gene 1996, V181, P113 CAPLUS
(5) Balm, P; General and Comparative Endocrinology 1994, V96, P347 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L13 ANSWER 29 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1998:326162 CAPLUS
DN 128:304680
TI Plastid genome characterization in parasitic plants - biological, genetic, taxonomic, and applied aspects
AU Thalouarn, Patrick; Delavault, Philippe; Lusson, Nathalie; Russo-Sorel, Nathalie; Theodet, Catherine; Benharrat, Hocine
CS Groupe Physiol. Pathol. vegetales, Univ. Nantes, Nantes, 44322, Fr.
SO C. R. Seances Soc. Biol. Ses Fil. (1998), 192(1), 53-73
CODEN: CRSBAW; ISSN: 0037-9026
PB SGS
DT Journal
LA French
AB Parasitic phanerogams receive water and assimilates essential for their growth from the host plant. Holoparasites, esp., do not have a functional photosynthetic app. and are entirely dependent on their host for reduced carbon. Nevertheless, hemiparasites, which are photosynthetic, could also rob the host plant of water, minerals, and even carbohydrates. As genetic information of the plastid genome is mostly located in genes coding for proteins involved in photosynthesis, the question is raised of their maintenance in parasitic plants. The first signs of a parasitism-related evolution appear in a hemiparasite like Striga hermonthica where not all the ndh genes coding for subunits of a NADPH plastoquinone oxidoreductase involved in chlororespiration are retained. Using heterologous probes representing the entire plastid genome of tobacco, we demonstrated that the plastid DNA from the holoparasitic Scrophulariaceae Lathraea clandestina is strongly reduced in size. Indeed, this circular DNA mol. is 110 kb long whereas that of tobacco is 155 kb in size. This is mainly due to the redn. of single copy regions which contain chlororespiratory and photosynthetic genes. Among these genes only rbcL which codes for the large subunit of Rubisco has been maintained in a functional form. This is not surprising since a weak Rubisco activity was previously demonstrated in Lathraea scale-leaves. The maintenance of the rbcL gene is likely the reason of the presence of most of the housekeeping genes, mainly on the inverted repeat region which is almost entirely conserved on Lathraea plastid DNA. Indeed, the expression of some housekeeping genes, like 16S RNA, rpl20 and rps7 was demonstrated. In contrast, the 4 RNA polymerase rpo genes on an Escherichia coli-like plastid were demonstrated to be pseudogenes. This feature implies that an alternative RNA polymerase must be active in Lathraea amyloplasts, for instance to transcribe the rbcL gene. As a matter of fact, the **nucleotide** sequence of its 5' upstream region shows that besides the E. coli-like -10 and -35 sequences there is another promoter which is usually found in the housekeeping genes of the chloroplast. Both plastid genome size and photosynthetic and chlororespiratory gene content redns. can easily be explained by the loss of photosynthetic function in holoparasites. However, the function of Rubisco in Lathraea remains unclear. Another question which arises from these results is related to the mechanism which compensates for the loss of some genes for tRNA, ribosomal proteins or

subunits of plastid-encoded RNA polymerase. Lastly a comparison of nuclear and plastid genes encoding for subunits of proteins found in the plastid has been undertaken. The authors' first results suggest that the evolution towards pseudogenes exhibiting a drastically modified **nucleotide** sequence has happened at a lower rate in the nucleus. In the Orobanchaceae, a family entirely consisting of holoparasites, the plastid genome is more reduced in size than in Lathraea and rbcL is not a pseudogene like all other non-housekeeping genees. Provided that they are not truncated nor too rearranged, pseudo genes could be interesting tools in taxonomy. For instance, the rbcL pseudogene differs in each species of the genus Orobanche which makes possible a clarification of taxonomy of some of its subsections.

L13 ANSWER 30 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1999:461482 CAPLUS
DN 131:267735
TI Mitochondrial genome organization and evolution within the green algae and land plants
AU Gray, M. W.; Lemieux, C.; Burger, G.; Lang, B. F.; Otis, C.; Plante, I.; Turmel, M.
CS Department of Biochemistry, Dalhousie University, Halifax, NS, B3H 4H7, Can.
SO Plant Mitochondria, Proc. Int. Congr. (1998), 1-8. Editor(s): Moller, Ian M. Publisher: Backhuys Publishers, Leiden, Neth.
CODEN: 67WYAZ
DT Conference
LA English
AB Complete sequences of the mitochondrial genomes of two green algae, Nephroselmis olivaceae and Pedinomonas minor (both prasinophytes), are compared and contrasted. The Nephroselmis mitochondrial genome is 45,223 bp in size and encodes an expanded repertoire of respiratory chain genes, a no. of ribosomal protein genes, a virtually complete set of tRNA genes, and eubacteria-like large subunit, small subunit, and 5S rRNA genes, as well as a gene for the RNA component of RNase P. The 25,137-bp mitochondrial genome of P. minor is peculiar in its highly asym. distribution of coding and non-coding regions. The results are interpreted within the framework of existing data on completely sequenced chlorophyte and land plant mitochondrial DNAs.
RE.CNT 22
RE
(1) Boer, P; Cell 1988a, V55, P399 CAPLUS
(2) Boer, P; Curr Genet 1988b, V14, P583 CAPLUS
(3) Boer, P; Curr Gent 1991, V19, P309 CAPLUS
(4) Burger, G; J Mol Biol 1995, V245, P522 CAPLUS
(5) Denovan-Wright, E; J Mol Biol 1994, V241, P298 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L13 ANSWER 31 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1997:757022 CAPLUS
DN 128:58298
TI Protein and gene sequences expressed during infection by Streptococcus pneumoniae
IN Black, Michael Terrance; Hodgson, John Edward; Knowles, David Justin Charles; Nicholas, Richard Oakley; Stodola, Robert King
PA Smithkline Beecham Corporation, USA; Smithkline Beecham Plc; Black, Michael Terrance; Hodgson, John Edward; Knowles, David Justin Charles; Nicholas, Richard Oakley; Stodola, Robert King
SO PCT Int. Appl., 482 pp.
CODEN: PIXXD2
DT Patent
LA English

FAN.CNT 2

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9743303	A1	19971120	WO 1997-US7950	19970514
	W: JP, US RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
	EP 934336	A1	19990811	EP 1997-925516	19970514
	R: BE, CH, DE, DK, FR, GB, IT, LI, NL				
	JP 2000508178	T2	20000704	JP 1997-540991	19970514

PRAI US 1996-17670 19960514
WO 1997-US7950 19970514

AB Newly identified polynucleotides, polypeptides encoded by such polynucleotides, the uses of such polynucleotides and polypeptides, as well as the prodn. of such polynucleotides and polypeptides and recombinant host cells transformed with the polynucleotides are provided. Thus, 262 DNA fragment sequences and 290 encoded protein sequences are provided that are expressed by Streptococcus pneumoniae strain 0100993 during infection. Because each of the DNA sequences contains an open reading frame (ORF) with appropriate initiation and termination codons, the encoded protein upon expression can be used as a target for the screening of antimicrobial drugs. This invention also relates to inhibiting the biosynthesis or action of such polynucleotides or polypeptides and to the use of such inhibitors in therapy.

L13 ANSWER 32 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1997:293882 CAPLUS
DN 127:14134
TI Cloning of rice gene for mitochondrial ribosomal protein **S11** and use of its signal peptide for transporting proteins into mitochondria
IN Kadowaki, Koichi; Hirai, Atsushi
PA Norin Suisansho Nogyo Seibutsu Shigen Kenkyusho, Japan
SO Jpn. Kokai Tokkyo Koho, 11 pp.
CODEN: JKXXAF
DT Patent
LA Japanese

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	JP 09084588	A2	19970331	JP 1995-248150	19950926
	JP 2884486	B2	19990419		

AB Gene rps11 encoding mitochondrial ribosomal protein **S11** (RPS11) was isolated from rice. The gene contains 2 introns. The N-terminal peptide of RPS11 can direct protein transport from cytoplasm into mitochondria. Methods for directing protein transport into mitochondria using the above signal protein are claimed.

L13 ANSWER 33 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1997:204071 CAPLUS
DN 126:196114
TI Cloning of the promoters of genes for S-ribonucleases of tomato for style-specific gene expression to confer self-incompatibility
IN Kim, Chung I.; Nam, Hong G.; Takagi, Masamichi; Kim, Chung I.
PA S. Korea
SO Jpn. Kokai Tokkyo Koho, 15 pp.
CODEN: JKXXAF
DT Patent
LA Japanese

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	JP 09028381	A2	19970204	JP 1995-187557	19950724

AB Disclosed are the promoter region-contg. genomic DNA fragments of S alleles in wild tomato (Lycopersicon peruvianum). Isolated are two genomic fragments that corresponded to cDNAs for **S11** and S12

RNases fr[redacted]a genomic library of L. peruvianum with the S11S12 genotype. The promot[redacted] regions of the genomic DNA fr[redacted]ents were identified. The promoters are useful in style-specific S-gene expression to confer self-incompatibility in tomato or other Solanaceae plants.

L13 ANSWER 34 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1997:357772 CAPLUS
DN 127:76742
TI Complete **nucleotide** sequence of the chloroplast genome from the green alga Chlorella vulgaris: The existence of genes possibly involved in chloroplast division
AU Wakasugi, Tatsuya; Nagai, Toshiyuki; Kapoor, Meenu; Sugita, Mamoru; Ito, Mari; Ito, Shiho; Tsudzuki, Junko; Nakashima, Keiko; Tsudzuki, Takahiko; Suzuki, Yasuhiko; Hamada, Akira; Ohta, tutomu; Inamura, Atsushi; Yoshinaga, Koichi; Sugiura, Masahiro
CS Cent. Gene Res., Nagoya Univ., Nagoya, 464-01, Japan
SO Proc. Natl. Acad. Sci. U. S. A. (1997), 94(11), 5967-5972
CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
AB The complete **nucleotide** sequence of the chloroplast genome (150,613 bp) from the unicellular green alga Chlorella vulgaris C-27 was detd. The genome contains no large inverted repeat and has one copy of rRNA gene cluster consisting of 16S, 23S, and 5S rRNA genes. It contains 31 tRNA genes, of which the tRNALeu(GAG) gene has not been found in land plant chloroplast DNAs analyzed so far. Sixty-nine protein genes and 8 ORFs conserved with those found in land plant chloroplasts have also been found. The most striking is the existence of 2 adjacent genes homologous to bacterial genes involved in cell division, minD and minE, which are arranged in the same order in Escherichia coli. This finding suggests that the mechanism of chloroplast division is similar to bacterial division. Other than minD and minE homologs, genes encoding ribosomal proteins L5, L12, L19, and S9 (rpl5, rpl12, rpl19, and rps9); a chlorophyll biosynthesis Mg chelating subunit (chlI); and elongation factor EF-Tu (tufA), which have not been reported from land plant chloroplast DNAs, are present in this genome. However, many of the new chloroplast genes recently found in red and brown algae have not been found in C. vulgaris. Furthermore, this algal species possesses two long ORFs related to ycf1 and ycf2 that are exclusively found in land plants. These observations suggest that C. vulgaris is closer to land plants than to red and brown algae.

L13 ANSWER 35 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1997:584258 CAPLUS
DN 127:259159
TI Identifying the major proteome components of Haemophilus influenzae type-strain NCTC 8143
AU Link, Andrew J.; Hays, Lara G.; Carmack, Edwin B.; Yates, John R., III
CS Dep. Molecular Biotechnology, Washington Univ., Seattle, WA, 98195, USA
SO Electrophoresis (1997), 18(8), 1314-1334
CODEN: ELCTDN; ISSN: 0173-0835
PB Wiley-VCH
DT Journal
LA English
AB With the completion of the H. influenzae Rd genomic sequence, the identity
is known of most of the theor. proteins in the proteome of this bacterium.
However, the most abundant components of the actual proteome are unknown. Using mass spectrometry and 2-dimensional gel electrophoresis (2-DE), the most abundant proteins were sequenced and analyzed obsd. in the ATCC ref. strain of H. influenzae, NCTC 8143 (303 of 400 Coomassie-stained 2-DE spots). To automate the identification of 2-DE spots, a liq. autosampler

was coupled to a microcolumn liq. chromatog. electrospray ionization tandem mass spectrometer capable of identifying 22 spots per day. From the 303 sequenced spots, 263 unique proteins were identified . Most of the abundant proteins lie in an isoelec. point range of pH 4-7 and a mol. mass range of 10-100 kDa. Of the obsd. proteins, the most abundant is the outer membrane protein P2. Based on variety and abundance, proteins involved in energy metab. and macromol. synthesis are the dominant classes of proteins. Unexpectedly, tryptophanase was identified as a highly abundant protein in the strain NCTC 8143 whose sequence is not present in the genome of the Rd strain. By searching the tandem mass spectra against the translated genomic sequence, several proteins were identified which were not annotated in the genomic sequence. Surprisingly, 22% of the identified 2-DE spots represent isoforms in which gene products with the same primary sequence have different obsd. pI and Mr, indicating that these proteins are post-translationally processed. Although most proteins' predicted and obsd. isoelec. points and mol. masses show reasonable concordance, the obsd. values for several proteins deviate from the predicted values. These anomalies may represent either highly processed proteins or misinterpretations of the genomic sequence. Using the technol. developed in this project, the protein expression of other strains of H. influenzae grown under different environmental conditions can be compared to identify differences in their proteomes.

L13 ANSWER 36 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1998:4361 CAPLUS
DN 128:136955
TI Analysis of the cluster of ribosomal protein genes in the plastid genome of a unicellular red alga Cyanidioschyzon merolae: translocation of the str cluster as an early event in the rhodophyte-chromophyte lineage of plastid evolution
AU Ohta, Niji; Sato, Naoki; Nozaki, Hisayoshi; Kuroiwa, Tsuneyoshi
CS Sch. Human Sci., Waseda Univ., Saitama, 359, Japan
SO J. Mol. Evol. (1997), 45(6), 688-695
CODEN: JMEVAU; ISSN: 0022-2844
PB Springer-Verlag New York Inc.
DT Journal
LA English
AB The **nucleotide** sequence of a cluster of ribosomal protein genes in the plastid genome of a unicellular red alga, Cyanidioschyzon merolae, which has been supposed to be the most primitive alga, was detd. The phylogenetic tree inferred from the amino acid sequence of ribosomal proteins of two rhodophytes, a chromophyte, a glaucophyte, two chlorophytes (land plants), a cyanobacterium, and three eubacteria suggested a close relationship between the cyanobacterium Synechocystis PCC6803 and the plastids of various species in the kingdom Plantae, which is consistent with the hypothesis of the endosymbiotic origin of plastids.
In this tree, the two species of rhodophytes were grouped with the chromophyte, and the glaucophyte was grouped with the chlorophytes. Anal. of the organization of the genes encoding the ribosomal proteins suggested that the translocation of the str cluster occurred early in the lineage of rhodophytes and chromophytes after these groups had been sepd. from chlorophytes and glaucophytes.

L13 ANSWER 37 OF 122 SCISEARCH COPYRIGHT 2000 ISI (R)DUPLICATE 5
AN 97:217149 SCISEARCH
GA The Genuine Article (R) Number: WM107
TI Cloning and characterization of a cDNA encoding a maize seedling phytase

AU Maugenest S; Martinez I; Lescure A M (Reprint)
CS INRA, INA, PG, LAB BIOL SEMENCES, F-78026 VERSAILLES, FRANCE (Reprint); INRA, INA, PG, LAB BIOL SEMENCES, F-78026 VERSAILLES, FRANCE; BIOCEM, GRP LIMAGRAIN, F-63170 CLERMONT FERRAN, FRANCE
CYA FRANCE
SO BIOCHEMICAL JOURNAL, (1 MAR 1997) Vol. 322, Part 2, pp. 511-517.
Publisher: PORTLAND PRESS, 59 PORTLAND PLACE, LONDON, ENGLAND W1N 3AJ.
ISSN: 0264-6021.
DT Article; Journal
FS LIFE
LA English
REC Reference Count: 43
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB During germination, maize seedlings express a phytase able to hydrolyse the large amount of phytin stored in the dry seed. Previous studies allowed purification and characterization of this enzyme as a homodimer of 38 kDa subunits [Laboure, Gagnon and Lescure, Biochem. J. (1993) 295, 413-419]. In the present work, an antibody against the purified maize phytase has been used to screen a maize seedling cDNA expression library. Several positive clones containing an insert of about 1400 bp were isolated. The **nucleotide** sequence of the insert of one of these clones has been established. This cDNA, called phy **S11**, was 1335 bp long and contained an open reading frame of 387 amino acids. The sequence of N-terminal residues (23 amino acids) of the purified phytase has been established. These residues are found at positions 19-41 of the amino acid sequence encoded by phy **S11**. This confirms that this cDNA codes for the maize phytase. The deduced amino acid sequence appears to be very different from those of published Aspergillus niger phytases; however, an homologous region of 33 amino acids was detected. This region of the fungal sequence contains the RHGxRxP consensus motif found in various high molecular mass acid phosphatases and believed to be the acceptor site for phosphate. Expression of the phy **S11** cDNA in Escherichia coli allowed the production of the phytase subunit and its assembly to give a protein of the same size as the native phytase. The time course of phy **S11** mRNA accumulation during germination showed that no transcript was present in dry seeds. The mRNA accumulated during the first day of germination, to reach a maximum after 2 days (radicle protrusion), and then decreased in young seedlings. Genomic Southern blot analyses suggest the existence of at least two genes and genetic mapping reveals two loci separated by 1 cM on chromosome 3 of maize. The cloning of this first cDNA coding for a plant phytase, will allow the isolation of the corresponding genes and the study of their regulation during germination.

L13 ANSWER 38 OF 122 SCISEARCH COPYRIGHT 2000 ISI (R)DUPLICATE 6
AN 97:640709 SCISEARCH
GA The Genuine Article (R) Number: XT078
TI Organization of a large gene cluster encoding ribosomal proteins in the cyanobacterium Synechococcus sp. strain PCC 6301: comparison of gene clusters among cyanobacteria, eubacteria and chloroplast genomes
AU Sugita M (Reprint); Sugishita H; Fujishiro T; Tsuboi M; Sugita C; Endo T; Sugiura M
CS NAGOYA UNIV, CTR GENE RES, NAGOYA, AICHI 46401, JAPAN (Reprint); NAGOYA UNIV, DEPT CHEM, NAGOYA, AICHI 46401, JAPAN
CYA JAPAN
SO GENE, (11 AUG 1997) Vol. 195, No. 1, pp. 73-79.
Publisher: ELSEVIER SCIENCE BV, PO BOX 211, 1000 AE AMSTERDAM, NETHERLANDS.
ISSN: 0378-1119.
DT Article; Journal
FS LIFE
LA English
REC Reference Count: 32

ABSTRACTS AVAILABLE IN THE ALL AND IALL FORMATS

AB The structure of a large gene cluster containing 22 ribosomal protein (r-protein) genes of the cyanobacterium Synechococcus sp. strain PCC6301 is presented. Based on DNA and protein sequence analyses, genes encoding r-proteins L3, L4, L23, L2, S19, L22, S3, L16, L29, S17, L14, L24, L5, S8, L6, L18, S5, L15, L36, S13, **S11**, L17, SecY, adenylate kinase (AK) and the alpha subunit of RNA polymerase were identified. The gene order is similar to that of the E, coli S10, spe and alpha operons. Unlike the corresponding E. coli operons, the genes for r-proteins S4, S10, S14 and L30 are not present in this cluster. The organization of Synechococcus r-protein genes also resembles that of chloroplast (cp) r-protein genes of red and brown algal species. This strongly supports the endosymbiotic theory that the cp genome evolved from an ancient photosynthetic bacterium. (C) 1997 Elsevier Science B.V.

L13 ANSWER 39 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1997:35019 CAPLUS
DN 126:140366
TI The mitochondrial genome of Arabidopsis thaliana contains 57 genes in 366,924 **nucleotides**
AU Unseld, Michael; Marienfeld, Joachim R.; Brandt, Petra; Brennicke, Axel
CS Inst. Genbiol. Forschung, Berlin, D-14195, Germany
SO Nat. Genet. (1997), 15(1), 57-61
CODEN: NGENEC; ISSN: 1061-4036
PB Nature Publishing Co.
DT Journal
LA English
AB The complete sequence of mitochondrial DNA was detd. in the model plant species Arabidopsis thaliana, affording access to the first of its 3 genomes. The 366,924 **nucleotides** code for 57 identified genes, which cover only 10% of the genome. Introns in these genes add .apprx.8%, open reading frames >100 amino acids represent 10% of the genome, duplications account for 7%, remnants of retrotransposons of nuclear origin contribute 4%, and integrated plastid sequences amt. to 1% - leaving 60% of the genome unaccounted for. With the significant contribution of duplications, imported foreign DNA and the extensive background of apparently functionless sequences, the mosaic structure of the Arabidopsis thaliana mitochondrial genome features many aspects of size-relaxed nuclear genomes.

L13 ANSWER 40 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1996:689784 CAPLUS
DN 126:2337
TI Identification and characterization of differentially expressed cDNAs of the vector mosquito, Anopheles gambiae
AU Dimopoulos, George; Richman, Adam; della Torre, Alessandra; Kafatos, Fotis C.; Louis, Christos
CS Found. Res. Technol.-Hellas, Inst. Mol. Biol. Biotechnol., Crete, GR-711 10, Greece
SO Proc. Natl. Acad. Sci. U. S. A. (1996), 93(23), 13066-13071
CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
AB The isolation and study of Anopheles gambiae genes that are differentially expressed in development, notably in tissues assocd. with the maturation and transmission of the malaria parasite, is important for the elucidation

of basic mol. mechanisms underlying vector parasite interactions. We have used the differential display technique to screen for mRNAs specifically expressed in adult males, females, and midgut tissues of blood-fed and unfed females. We also screened for mRNAs specifically induced upon bacterial infection of larval stage mosquitoes. We have characterized 19 distinct cDNAs, most of which show developmentally regulated expression specificity during the mosquito life cycle. The most interesting are six new sequences that are midgut-specific in the adult, three of which are also modulated by blood-feeding. The gut-specific sequences encode a maltase, a V-ATPase subunit, a GTP binding protein, two different lectins, and a nontrypsin serine protease. The latter sequence is also induced in larvae subjected to bacterial challenge. With the exception of a mitochondrial DNA fragment, the other 18 sequences constitute expressed genomic sequence tags, 4 of which have been mapped cytogenetically.

L13 ANSWER 41 OF 122 SCISEARCH COPYRIGHT 2000 ISI (R)DUPLICATE 7
AN 97:30428 SCISEARCH
GA The Genuine Article (R) Number: VZ409
TI Targeting presequence acquisition after mitochondrial gene transfer to the nucleus occurs by duplication of existing targeting signals
AU Kadowaki K I (Reprint); Kubo N; Ozawa K; Hirai A
CS NATL INST AGROBIOL RESOURCES, DEPT MOL BIOL, TSUKUBA, IBARAKI 305, JAPAN (Reprint); UNIV TOKYO, FAC AGR, TOKYO 113, JAPAN
CYA JAPAN
SO EMBO JOURNAL, (2 DEC 1996) Vol. 15, No. 23, pp. 6652-6661.
Publisher: OXFORD UNIV PRESS UNITED KINGDOM, WALTON ST JOURNALS DEPT, OXFORD, ENGLAND OX2 6DP.
ISSN: 0261-4189.
DT Article; Journal
FS LIFE
LA English
REC Reference Count: 37
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS
AB We have cloned a gene for mitochondrial ribosomal protein **S11** (RPS11), which is encoded in lower plants by the mitochondrial genome, in higher plants by the nuclear genome, demonstrating genetic information transfer from the mitochondrial genome to the nucleus during flowering plant evolution, The sequence **s11**-1 encodes an N-terminal extension as well as an organelle-derived RPS11 region, Surprisingly, the N-terminal region has high amino acid sequence similarity with the presequence of the beta-subunit of ATP synthase from plant mitochondria, suggesting a common lineage of the presequences, The deduced N-terminal region of **s11**-2, a second nuclear-encoded homolog of rps11, shows high sequence similarity with the putative presequence of cytochrome oxidase subunit Vb. The sharing of the N-terminal region together with its 5' flanking untranslated **nucleotide** sequence in different proteins strongly suggests an involvement of duplication/recombination for targeting signal acquisition after gene migration, A remnant of ancestral rps11 sequence, transcribed and subjected to RNA editing, is found in the mitochondrial genome, indicating that inactivation of mitochondrial rps11 gene expression was initiated at the translational level prior to termination of transcription.

L13 ANSWER 42 OF 122 SCISEARCH COPYRIGHT 2000 ISI (R)DUPLICATE 8
AN 96:908224 SCISEARCH
GA The Genuine Article (R) Number: VW528
TI Molecular analysis of RNA polymerase alpha subunit gene from Streptomyces coelicolor A3(2)
AU Cho E J; Bae J B; Kang J G; Roe J H (Reprint)

CS HARVARD UNIV, SCH MED, DEPT BIOL CHEM & MOL PHARMACOL, BOSTON, MA 02115 (Reprint) SEOUL NATL UNIV, COLL NAT SCI, DEPT MICROBIOL, SEOUL 151742, SOUTH KOREA; SEOUL NATL UNIV, COLL NAT SCI, RES CTR MOL MICROBIOL, SEOUL 151742, SOUTH KOREA
CYA USA; SOUTH KOREA
SO NUCLEIC ACIDS RESEARCH, (15 NOV 1996) Vol. 24, No. 22, pp. 4565-4571. Publisher: OXFORD UNIV PRESS UNITED KINGDOM, WALTON ST JOURNALS DEPT, OXFORD, ENGLAND OX2 6DP.
ISSN: 0305-1048.
DT Article; Journal
FS LIFE
LA English
REC Reference Count: 50
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB The rpoA gene, encoding the alpha subunit of RNA polymerase, was cloned from Streptomyces coelicolor A3(2). It is preceded by rpsK and followed by rpIQ, encoding ribosomal proteins **S11** and L17, respectively, similar to the gene order in Bacillus subtilis, The rpoA gene specifies a protein of 339 amino acids with deduced molecular mass of 36 510 Da, exhibiting 64.3 and 70.7% similarity over its entire length to Escherichia coil and B. subtilis alpha subunits, respectively. Using T7 expression system, we overexpressed the S. coelicolor alpha protein in E. coli. A small fraction of this protein was found to be assembled into E. coli RNA polymerase, Antibody against S. coelicolor a protein crossreacted with that of B. subtilis move than with the E. coli alpha subunit, The ability of recombinant a protein to assemble beta and beta' subunits into core enzyme in vitro was examined by measuring the core enzyme activity, Maximal reconstitution was obtained at alpha(2):beta+beta' ratio of 1:2.3, indicating that the recombinant ex protein is fully functional for subunit assembly, Similar results were also obtained for natural alpha protein, Limited proteolysis with endoproteinase Glu-C revealed that S. coelicolor alpha contains a tightly folded N-terminal domain and the C-terminal region is more protease-sensitive than that of E. coli alpha.

L13 ANSWER 43 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1996:729783 CAPLUS
DN 126:85324
TI Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae
AU Himmelreich, Ralf; Hilbert, Helmut; Plagens, Helga; Pirkl, Elsbeth; Li, Bi-Chen; Herrmann, Richard
CS Zenatrum Mol. Biologie Heidelberg, Univ. Heidelberg, Heidelberg, 69120, Germany
SO Nucleic Acids Res. (1996), 24(22), 4420-4449
CODEN: NARHAD; ISSN: 0305-1048
PB Oxford University Press
DT Journal
LA English

AB The entire genome of the bacterium Mycoplasma pneumoniae M129 has been sequenced. It has a size of 816 394 base pairs with an av. G+C content of 40.0 mol%. We predict 677 open reading frames (ORFs) and 39 genes coding for various RNA species. Of the predicted ORFs, 75.9% showed significant similarity to genes/proteins of other organisms while only 9.9% did not reveal any significant similarity to gene sequences in databases. This permitted us tentatively to assign a functional classification to a large no. of ORFs and to deduce the biochem. and physiol. properties of this bacterium. The redn. of the genome size of M. pneumoniae during its reductive evolution from ancestral bacteria can be explained by the loss of complete anabolic (e.g. no amino acid synthesis) and metabolic

pathways. Therefore, M. pneumoniae depends in nature on an obligate parasitic lifestyle which requires the provision of exogenous essential metabolites. All the major classes of cellular processes and metabolic pathways are briefly described. For a no. of activities/functions present in M. pneumoniae according to exptl. evidence, the corresponding genes could not be identified by similarity search. For instance we failed to identify genes/proteins involved in motility, chemotaxis and management of oxidative stress.

L13 ANSWER 44 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1996:554294 CAPLUS
DN 125:213846
TI Molecular cloning of a RNA-binding protein, S1-1
AU Inoue, Akira; Paulo, Kenichi; Kimura, Masatsugu; Watanabe, Takanori; Morisawa, Seiji
CS Dep. Biochem., Osaka City Univ. Med. Sch., Osaka, 545, Japan
SO Nucleic Acids Res. (1996), 24(15), 2990-2997
CODEN: NARHAD; ISSN: 0305-1048
DT Journal
LA English
AB S1 proteins A-D constitute a nuclear protein family that are liberated rapidly in a set from chromatin by mild digestion with a DNA or RNA hydrolyzing enzyme. With an anti-S1-protein B antiserum that reacted with B2, C1 and D1, a cDNA clone, pS1-1, was obtained, which encoded a protein of 852 amino acids. The S1-1 protein, encoded within the cells by a mRNA of 3480 nt, was a novel protein and could be distinguished from the S1 proteins B, C and D by their amino acid sequences. The S1-1 protein synthesized by in vitro translation bound to RNA homopolymers, with a preference for G and U polyribonucleotides and little for poly(A). The protein contained two tandem RNP motifs and several intriguing sequences, such as a novel repeat of five octamers with a consensus sequence DP-S(Q/G)YYY and a potentially perfect amphipathic .alpha.-helix of five turns with basic and acidic amino acids positioned in an ordered way. The two RNP motif sequences were similar, although homologies were low, to the RNP motif sequences of yeast NSR1 protein, animal nucleolins, Drosophila hnRNP A1 and tobacco chloroplast RNP precursor protein, suggesting a functional uniqueness of the S1-1 protein in RNA metab. and also the evolution of its RNP motif structure before plants and animals diverged. These results indicate that the S1-1 protein encoded by the cDNA is a new class of RNA-binding protein.

L13 ANSWER 45 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1996:140546 CAPLUS
DN 124:252169
TI Sequence analysis of 56 kb from the genome of the bacterium Mycoplasma pneumoniae comprising the dnaA region, the atp operon and a cluster of ribosomal protein genes
AU Hilbert, Helmut; Himmelreich, Ralf; Plagens, Helga; Herrmann, Richard
CS Zentrum Mol. Biol. Heidelberg Mikrobiol., Univ. Heidelberg, Heidelberg, 69120, Germany
SO Nucleic Acids Res. (1996), 24(4), 628-39
CODEN: NARHAD; ISSN: 0305-1048
DT Journal
LA English
AB To sequence the entire 800 kb pair genome of the bacterium Mycoplasma pneumoniae, a plasmid library was established which contained the majority of the EcoRI fragments from M. pneumoniae. The EcoRI fragments were subcloned from an ordered cosmid library comprising the complete M. pneumoniae genome. Individual plasmid clones were sequenced in an ordered

fashion only by primer walking. This report describes the initial results from the sequence anal. of .apprx kb comprising the dnaA region as a potential origin of replication, the ATPase operon, and a region coding for a cluster of ribosomal protein genes. The data were compared with the corresponding genes/operons from Bacillus subtilis, Escherichia coli, Mycoplasma capricolum, and Mycoplasma gallisepticum.

L13 ANSWER 46 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1996:201394 CAPLUS
DN 124:280616
TI An expressed sequence tag analysis of a full-length, spliced-leader cDNA library from Leishmania major promastigotes
AU Levick, Mark P.; Blackwell, Jenefer M.; Connor, Vivienne; Coulson, Richard M. R.; Miles, Alistair; Smith, Heather E.; Wan, Kiew-Lian; Ajioka, James W.
CS Department of Pathology, University of Cambridge, Tennis Court Road, Cambridge, CB2 1QP, UK
SO Mol. Biochem. Parasitol. (1996), 76(1,2), 345-8
CODEN: MBIPDP; ISSN: 0166-6851
DT Journal
LA English
AB A directionally cloned, full-length, spliced-leader cDNA library was constructed from promastigotes of Leishmania major and characterized by expressed sequence tag (EST) anal. The 5' spliced-leader sequence was present in >99% of the ESTs. Of the 268 analyzed ESTs, 74 (27.6%) were assigned a putative identity, based on significant protein or noncoding nucleic acid matches, and the remaining 194 (72.4%) did not have significant matches and were classified as unidentified. The overall diversity was 74% and the overall redundancy was 26%.

L13 ANSWER 47 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1996:101135 CAPLUS
DN 124:167077
TI Genes for two subunits of succinate dehydrogenase form a cluster on the mitochondrial genome of Rhodophyta
AU Viehmann, Susanne; Richard, Odile; Boyen, Catherine; Zetsche, Klaus
CS Institut Pfanzenphysiologie, Justus-Liebig-Universitaet, Giessen, D-35392, Germany
SO Curr. Genet. (1996), 29(2), 199-201
CODEN: CUGED5; ISSN: 0172-8083
DT Journal
LA English
AB Mitochondrial DNA from the unicellular rhodophyte Cyanidium caldarium RK-1 and the multicellular Chondrus crispus were isolated, cloned, and sequenced. Two genes, sdhB and sdhC, that encode subunits of the succinate dehydrogenase, were identified by similarity. These genes form a cluster (sdhCB) in both red algae.

L13 ANSWER 48 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1996:214180 CAPLUS
DN 124:306597
TI Overproduction of mycobacterial ribosomal protein S13 induces catalase/peroxidase activity and hypersensitivity to isoniazid in Mycobacterium smegmatis
AU Dubnau, Eugenie; Soares, Sonia; Huang, Tian Jun; Jacobs, William R. Jr.
CS Public Health Research Institute, Tuberculosis Center, New York, NY, 10016, USA
SO Gene (1996), 170(1), 17-22
CODEN: GENED6; ISSN: 0378-1119
DT Journal
LA English

AB A Bacill[redacted] Calmette Guerlin (BCG) DNA fra[redacted]ent was identified which conferre[redacted]ypersensitivity to isoniazid ([redacted]) upon Mycobacterium smegmatis (Ms) when present on a multicopy plasmid. The gene cluster present on this fragment contains the genes encoding ribosomal proteins L36 (rpmJ), S13 (rpsM), **S11** (rpsK) and S4 (rpsD), as well as the gene encoding initiation factor-1 (infA), an open reading frame of unknown function (ORFX) and a putative promoter region. The rpsM gene, from either BCG or Ms is necessary and sufficient to produce the INH-hypersensitive phenotype in Ms, but the gene cluster has no effect on INH sensitivity when introduced into BCG on a multicopy plasmid. The presence of rpsM on a multicopy plasmid also causes an increase in catalase/peroxidase (Kat/Prx) activity in Ms. The overprodn. of S13 may induce a stress response, resulting in increased expression of katG (encoding Kat/Prx) in Ms, thereby causing hypersensitivity to INH.

L13 ANSWER 49 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1996:142744 CAPLUS
DN 124:252184
TI Genetic and transcriptional organization of the Bacillus subtilis spc-.alpha. region
AU Suh, Joo-Won; Boylan, Sharon A.; Oh, Se-Hoon; Price, Chester W.
CS Department of Food Science and Technology, University of California, Davis, CA, 95616, USA
SO Gene (1996), 169(1), 17-23
CODEN: GENED6; ISSN: 0378-1119
DT Journal
LA English
AB We used chromosomal walking methods to isolate a 10.8-kb region from the major ribosomal protein (r-protein) gene cluster of Bacillus subtilis (Bs). The gene order in this region, given by gene product, was r-proteins L16-L29-S17-L14-L24-L5-S14-S8-L6-L18-S5-L30-L15-SecY-adenylate kinase (Adk)-methionine aminopeptidase (Map)-initiation factor 1 (IF1)-L36-S13-**S11**-.alpha. subunit of RNA polymerase-L17. The region cloned, therefore, contains the homologues for the last three genes of the Escherichia coli (Ec) S10 operon, together with entire spc and .alpha. operons. This Bs organization differs from the corresponding region in Ec by the inclusion of the genes encoding Adk, Map and IF1 between the genes encoding SecY and L36. Plasmid integration expts. indicated that all 22 genes comprise a single large transcriptional unit controlled from a major promoter which lies upstream from the gene encoding r-protein L16. Promoter probe expts. located lesser activities internal to this large transcriptional unit, the secY and map promoters. The secY promoter region (psecY) contained two activities, each principally functioning in the stationary growth phase when high protein export is required. Thus, the Bs S10-spc-.alpha. region differs from its Ec counterpart in both genetic and transcriptional organization. Given this difference in transcriptional organization, the mechanisms coordinating expression of the translational app. are also likely to differ between Ec and Bs.

L13 ANSWER 50 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1996:575701 CAPLUS
DN 125:243324
TI Coat protein-mediated resistance to tomato mosaic virus in systemic and local lesion hosts
AU Yeh, Shyi-Dong; Pon, Jui-Chu
CS Dept. of Plant Pathology, National Chung Hsing Univ., Taichung, Taiwan
SO Zhiwu Bingli Xuehuikan (1996), 5(1), 15-27
CODEN: ZBXUFM; ISSN: 1021-9544
DT Journal
LA English
AB Tomato mosaic virus (ToMV) is widespread and often epidemic in tomato and pepper crops in Taiwan. A cDNA clone pTCP was obtained from RT-PCR

amplification of ToMV RNA of a virus isolate originated from tomato. The complete **nucleotide** sequence of the coat protein (CP) gene of ToMV was detd. from subclones of restriction enzyme fragments of pTCP. The clone pTCP covered the entire CP gene that contained 690 **nucleotides** in length with a capacity encoding a protein of 158 amino acids. Comparison of the nucleic acid sequence of the CP gene of the Taiwan ToMV with that of the published Japan isolate showed that there were three **nucleotides** different and the amino acid sequences of the CP genes of both isolates are identical, indicating that the Taiwan ToMV is almost identical to the Japan ToMV. In vitro translation from the in vitro transcript generated from pTCP produced a protein with a Mr of 17.5 kDa which reacted specifically with the antibody to the ToMV CP. The ToMV CP fragment was digested from pTCP and subcloned in the Ti binary vector, and used for transformation of tobaccos, including the local lesion host of Nicotiana tabacum cv. Havana and the systemic hosts of N. tabacum cv. Samsun and cv. Xanthi. There were 20 transgenic tobacco lines regenerated, including 6 lines of Havana (T2, T3, T8, T11, T12 and T15), 5 lines Xanthi (X1, X2, X4, X5 and X7) and 9 lines of Samsun (S1, S2, S3, S6, S8, S9, S10, **S11** and S12). The presence of the ToMV CP cDNA in the putative transgenic plants was confirmed by PCR using primers specific to the CP gene. A protein product similar to ToMV-CP was detected in the transgenic plants when they were analyzed by Western blotting and indirect ELISA. When the transgenic Havana plants were inoculated with ToMV at 1 .mu.g/mL, the nos. of local lesions were only 18-21% as compared with those on untransformed tobacco. In systemic hosts, symptom development was delayed 3-18 days as compared with the control after they were inoculated with ToMV at 0.5 .mu.g/mL. The construction of the ToMV CP-transgenic tobacco plants resistant to ToMV infection provided a model system for control of diseases caused by ToMV in tomato, sweet pepper and chili pepper in Taiwan.

L13 ANSWER 51 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1995:545698 CAPLUS
DN 123:26941
TI Cloning and characterization of the RNA polymerase .alpha.-subunit operon of Chlamydia trachomatis [Erratum to document cited in CA120:126406]
AU Tan, Ming; Klein, Russell; Grant, Richard; Ganem, Don; Engel, Joanne
CS Dep. Microbiol. Immunology Med., Univ. California, San Francisco, San Francisco, CA, 94143, USA
SO J. Bacteriol. (1995), 177(9), 2607
CODEN: JOBAAY; ISSN: 0021-9193
DT Journal
LA English
AB The errors were reflected in the abstr. and the index entries.

L13 ANSWER 52 OF 122 SCISEARCH COPYRIGHT 2000 ISI (R)DUPLICATE 9
AN 95:331535 SCISEARCH
GA The Genuine Article (R) Number: QW529
TI CHLAMYDIA-TRACHOMATIS RNA-POLYMERASE ALPHA-SUBUNIT - SEQUENCE AND STRUCTURAL-ANALYSIS
AU GU L J; WENMAN W M; REMACHA M; MEUSER R; COFFIN J; KAUL R (Reprint)
CS UNIV CALIF DAVIS, DEPT PEDIAT, 201 NEUROSCI BLDG, 1515 NEWTON CT, DAVIS, CA, 95616 (Reprint); UNIV CALIF DAVIS, DEPT PEDIAT, DAVIS, CA, 95616; UNIV ALBERTA, DEPT PEDIAT, DIV INFECT DIS, EDMONTON, AB T6G 2R7, CANADA
CYA USA; CANADA
SO JOURNAL OF BACTERIOLOGY, (MAY 1995) Vol. 177, No. 9, pp. 2594-2601. ISSN: 0021-9193.
DT Note; Journal
FS LIFE

LA ENGLISH
REC Reference count: 48
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB We describe the cloning and sequence analysis of the region surrounding the gene for the alpha subunit of RNA polymerase from Chlamydia trachomatis. This region contains genes for proteins in the order SecY, S13, **S11**, alpha, and L17, which are equivalent to Escherichia coli and Bacillus subtilis r proteins. The incorporation of chlamydial alpha subunit protein into the E. coli RNA polymerase holoenzyme rather than its truncated variant lacking the amino terminus suggests the existence of structural conservation among alpha subunits from distantly related genera.

L13 ANSWER 53 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1995:1006044 CAPLUS
DN 124:78239
TI The 5' flanking sequences of two S alleles in Lycopersicon peruvianum are highly heterologous but contain short blocks of homologous sequences
AU Chung, Il Kyung; Lee, Sang Yeb; Ito, Toru; Tanaka, Hiroshi; Nam, Hong Gil; Takagi, Masamichi
CS Dep. Life Sci., Pohang Univ. Sci. Technol., Pohang, 790-784, S. Korea
SO Plant Cell Physiol. (1995), 36(8), 1621-7
CODEN: PCPHA5; ISSN: 0032-0781
DT Journal
LA English
AB To characterize the mol. structure of the S alleles in Lycopersicon peruvianum, we isolated two genomic fragments that corresponded to cDNAs for **S11** and S12 RNases from a genomic library of a plant with the S11S12 genotype. The coding regions and the flanking regions in both fragments were sequenced. A single short intron was found in each gene for RNase, and it was located in the previously identified HV2 region [Chung et al. (1994) Plant Mol. Biol. 26: 757]. The site of initiation of transcription of the gene for **S11** RNase was detd. by a primer extension anal. and a putative TATA box was identified. Three short sequences that were highly homologous in the two S alleles were found within 360 bp upstream of the ATG initiation codon. It is suggested that these sequences might be involved in the regulation of transcription required for the appropriate-level or tissue-specific expression of the S genes in L. peruvianum.

L13 ANSWER 54 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1995:713131 CAPLUS
DN 124:22808
TI Complete sequence of the mitochondrial DNA of the rhodophyte Chondrus crispus (Gigartinales). Gene content and genome organization
AU Leblanc, Catherine; Boyen, Catherine; Richard, Odile; Bonnard, Geraldine; Grienenberger, Jean-Michel; Kloareg, Bernard
CS Cent. Etudes Oceanologiques Biol. Marine, Univ. P. & M. Curie, Roscoff, 29682, Fr.
SO J. Mol. Biol. (1995), 250(4), 484-95
CODEN: JMOBAK; ISSN: 0022-2836
DT Journal
LA English
AB The complete **nucleotide** sequence of the circular mitochondrial (mt) DNA from the red alga Chondrus crispus was detd. (25,836 **nucleotides**, A + T content 72.1%). Fifty-one genes were identified. They include genes encoding 3 subunits of the cytochrome oxidase (cox1 to 3), apocytochrome b (cob), 7 subunits of the NADH dehydrogenase complex (nad1 to 6, nad4L), two ATPase subunits (atp6 and atp9), three rRNAs (rrn5, srn, and Lrn), 23 tRNAs, and 4 ribosomal proteins (rps3, rps11, rps12, and rpl16). Two subunits of the succinate dehydrogenase complex (sdhB and sdhC), usually found on nuclear genomes,

are also located on the mtDNA of C. crispus. One group IIb intron is inserted in the tRNAIle gene. Six potentially functional open reading frames were identified, 4 of them having counterparts among green plant mtDNAs. The use of a modified genetic code and the absence of RNA editing, previously reported for the cox3 gene, appears as a general characteristic of this mol. Mitochondrial genes are encoded on both DNA strands, in 2 opposite major transcriptional directions, suggesting the existence of 2 main transcriptional units. Two long and stable stem-loops were identified in intergenic regions, which are believed to be involved with transcription and replication. The main structural features of this genome are compared with the overall organization of mtDNAs and are discussed in view of the evolution of mitochondria.

L13 ANSWER 55 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1996:111518 CAPLUS
DN 124:195299
TI **Nucleotide** sequence of the cyanelle genome from Cyanophora paradoxa
AU Stirewalt, Veronica L.; Michalowski, Christine B.; Loeffelhardt, Wolfgang;
Bohnert, Hans J.; Bryant, Donald A.
CS Department of Biochemistry and Molecular Biology, Pennsylvania State University, University Park, PA, 16802, USA
SO Plant Mol. Biol. Rep. (1995), Volume Date 1995, 13(4), 327-32
CODEN: PMBRD4; ISSN: 0735-9640
DT Journal
LA English
AB The complete **nucleotide** sequence of the cyanelle genome of Cyanophora paradoxa Pringsheim strain LB 555 was detd. (GenBank Accession No. U30821). The circular mol. is 135,599 base pairs in length. The phys. map of this DNA mol. is shown along with identified genes and open reading frames.

L13 ANSWER 56 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1995:926867 CAPLUS
DN 124:23005
TI cDNA cloning and sequence analysis of rice dwarf virus genome segment S9
AU Qu, Lin; Li, Yi; Zhu, Yuxian; Chen, Zhangliang
CS Coll. Life Sci., Peking Univ., Beijing, 100871, Peop. Rep. China
SO Bingdu Xuebao (1995), 11(3), 271-5
CODEN: BIXUEA; ISSN: 1000-8721
DT Journal
LA Chinese
AB The cDNA of Rice Dwarf Virus (RDV) Fujian isolate genome segment S9 was synthesized and amplified by RT-PCR. The PCR product was cloned and sequenced. The cloned fragment is 1,225bp in length, encodes a 39kD protein. This fragment has 93.9% homol. in **nucleotide** sequence and 91.7% in amino acid sequence with RDV Japanese isolate S9. Amino acid sequence comparison also showed that the N-terminal region of 39 kD protein is highly conserved. It may suggest that the N-terminal regions plays an important role in vivo in virus replication and encapsidation. Amino acid sequence comparison of proteins encoded by RDV S9 and WTV **S11** also showed 32.9% homol.

L13 ANSWER 57 OF 122 SCISEARCH COPYRIGHT 2000 ISI (R)DUPLICATE 10
AN 95:391893 SCISEARCH
GA The Genuine Article (R) Number: RA710
TI MOLECULAR ANALYSIS OF THE RICE DWARF VIRUS GENOME
AU SUZUKI N (Reprint)
CS AKITA PREFECTURAL COLL AGR, INST BIOTECHNOL, PLANT GENET ENGN LAB, AKITA 01004, JAPAN (Reprint)
CYA JAPAN
SO SEMINARS IN VIROLOGY, (APR 1995) Vol. 6, No. 2, pp. 89-95.

ISSN: 1044-5773.
DT Article; Journal
FS LIFE
LA ENGLISH
REC Reference Count: 60
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS
AB Sequences of all 12 rice dwarf phytoreovirus (RDV) genome segments (S1-S12) have been determined. Each segment has a terminal sequence of six 5'- and four 3'-**nucleotides** conserved in all segments, and a subterminal segment-specific inverted repeat. RDV S1 to **S11** each contain single large open reading frames (ORFs), while S12 has three potential ORFs and specifies three polypeptides in vitro. The following gene product assignments have been established: S1-S3 S5, S7 and S8 encode structural proteins, and S4, S6 and S9-S12 code for non-structural ones. Data on functions of some of the gene products, and molecular evolution are also presented. These provide a basis for further molecular analysis of RDV.

L13 ANSWER 58 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1994:262683 CAPLUS
DN 120:262683
TI New albumin gene 3' adjacent to the .alpha.1-fetoprotein locus
AU Belanger, Luc; Roy, Sylvie; Allard, Denis
CS Cent. Rech. Cancerol., Univ. Laval, Quebec, PQ, G1R 2J6, Can.
SO J. Biol. Chem. (1994), 269(8), 5481-4
CODEN: JBCHA3; ISSN: 0021-9258
DT Journal
LA English
AB The albumin multigene family encodes proteins synthesized in the liver and secreted in the serum to fulfill ligand-carrier functions. The albumin (ALB), .alpha.1-fetoprotein (AFP), and vitamin D-binding protein genes are syntenic, the ALB and AFP genes are organized in tandem, and the AFP gene is selectively expressed in the fetal liver. The authors now report the existence of a fourth member of the albumin gene family, located 10 kilobases downstream from the AFP locus. The new gene, named .alpha.-albumin (.alpha.ALB), is selectively expressed in the liver at late stages of development. The .alpha.ALB mRNA sequence encodes a predicted secreted protein with the typical triple domain disulfide cross-linked structure. Comparisons of coding and promoter sequences suggest that .alpha.ALB could be a phylogenetic intermediate between the ALB and AFP genes. The developmental switch between .alpha.ALB gene activation and AFP gene repression suggests new regulatory interplays at the albumin locus and adult stage-specific ligand binding functions carried out by the .alpha.ALB gene product.

L13 ANSWER 59 OF 122 SCISEARCH COPYRIGHT 2000 ISI (R)
AN 94:408666 SCISEARCH
GA The Genuine Article (R) Number: NU205
TI THE DECODING REGION OF 16S RNA - A CROSS-LINKING STUDY OF THE RIBOSOMAL A-SITE, P-SITE AND E-SITE USING TRANSFER-RNA DERIVATIZED AT POSITION-32 IN THE ANTICODON LOOP
AU DORING T; MITCHELL P; OSSWALD M; BOCHKARIOV D; BRIMACOMBE R (Reprint)
CS MAX PLANCK INST MOLEC GENET, IHNESTR 73, D-14195 BERLIN, GERMANY (Reprint); MAX PLANCK INST MOLEC GENET, D-14195 BERLIN, GERMANY
CYA GERMANY
SO EMBO JOURNAL, (01 JUN 1994) Vol. 13, No. 11, pp. 2677-2685.
ISSN: 0261-4189.
DT Article; Journal
FS LIFE
LA ENGLISH

REC Reference count: 39
ABSTRACTS AVAILABLE IN THE ALL AND ... IAL ... ORMATS

AB A photo-reactive diazirine derivative was attached to the 2-thiocytidine residue at position 32 of tRNA(Arg)I from Escherichia coli. This modified tRNA was bound under suitable conditions to the A, P or E site of E.coli ribosomes. After photo-activation of the diazirine label, the sites of cross-linking to 16S rRNA were identified by our standard procedures. Each of the three tRNA binding sites showed a characteristic pattern of cross-linking. From tRNA at the A site, a major cross-link was observed to position 1378 of the 16S RNA, and a minor one to position 936. From the P site, there were major cross-links to positions 693 and to 957 and/or 966, as well as a minor cross-link to position 1338. The E site bound tRNA showed major cross-links to position 693 (identical to that from the P site) and to positions 1376/1378 (similar, but not identical, to the cross-link observed from the A site). Immunological analysis of the concomitantly cross-linked ribosomal proteins indicated that S7 was the major target of cross-linking from all three tRNA sites, with **S11** as a minor product. The results are discussed in terms of the overall topography of the decoding region of the 30S ribosomal subunit.

L13 ANSWER 60 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1994:647653 CAPLUS
DN 121:247653
TI A cDNA for Dunaliella tertiolecta cytosol ribosomal protein **S11**
AU LaRoche, Jolie; Wyman, Kevin; Falkowski, Paul G.
CS Dep. Appl. Sci., Brookhaven Natl. Lab., Upton, NY, 11973, USA
SO Plant Physiol. (1994), 105(4), 1447-8
CODEN: PLPHAY; ISSN: 0032-0889
DT Journal
LA English
AB All components of eukaryotic ribosomes are highly conserved throughout the taxonomic kingdom. Previously, there has been no sequence data available for lower photosynthetic eukaryotes. The authors have isolated and sequenced a cDNA clone pDTs11a encoding an **S11** ribosomal protein in a marine chlorophyte, Dunaliella tertiolecta. The EcoRI insert from the .lambda.gt11 clone was subcloned in M13mp19 in both orientations and the single-stranded DNA was sequenced by the dideoxy chain-termination method. The nucleic acid and amino acid sequences are 692 bp and 158 amino acids, resp. The 5' untranslated region is only 38 **nucleotides** long, whereas the 3' untranslated region is 185 **nucleotides** long. The codon usage in this gene is biased towards codons ending in C and G. The coding region predicts a protein that is approx. 17 kD. The **S11** ribosomal protein from D. tertiolecta has 67 and 64 % similarity with those of A. thaliana and rat, resp. In comparison, similarities among known higher-plant **S11** ribosomal proteins are greater than 80%.

L13 ANSWER 61 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1994:571834 CAPLUS
DN 121:171834
TI Ribosomal protein **S11** genes from Arabidopsis and soybean
AU Lenvik, Todd R.; Key, Joe L.; Gantt, J. Stephen
CS Dep. Plant Biol., Univ. Minnesota, St. Paul, MN, 55108, USA
SO Plant Physiol. (1994), 105(3), 1027-8
CODEN: PLPHAY; ISSN: 0032-0889
DT Journal
LA English
AB To begin a search for cis-acting elements that might be important for ribosomal protein gene regulation, the sequences were detd. for one of the genes (rps11) encoding ribosomal protein **S11** in Arabidopsis

thaliana and a homologous soybean gene. Both genes have 5 introns that are located in identical sites in the protein coding region and encode polyadenylated transcripts. Both genes also contain a telomere repeat sequence (TTAGGGT) located near the site of transcriptional initiation.

L13 ANSWER 62 OF 122 SCISEARCH COPYRIGHT 2000 ISI (R)DUPLICATE 11
AN 94:601390 SCISEARCH
GA The Genuine Article (R) Number: PG801
TI XENOPUS-LAEVIS RIBOSOMAL-PROTEIN **S11** - CLONING AND SEQUENCING OF THE CDNA AND PRIMARY STRUCTURE OF THE PROTEIN
AU ANNESI F; VESPIGNANI I; AMALDI F (Reprint); MARIOTTINI P
CS UNIV ROMA TOR VERGATA, DIPARTIMENTO BIOL, I-00133 ROME, ITALY (Reprint); UNIV ROMA TOR VERGATA, DIPARTIMENTO BIOL, I-00133 ROME, ITALY; UNIV PARMA, IST SCI BIOCHIM, I-43100 PARMA, ITALY
CYA ITALY
SO BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (15 SEP 1994) Vol. 203, No. 2, pp. 768-772.
ISSN: 0006-291X.
DT Article; Journal
FS LIFE
LA ENGLISH
REC Reference Count: 22
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS
AB We have cloned a Xenopus laevis cDNA coding for the 40S subunit cytoplasmic ribosomal protein **S11**. The **nucleotide** sequence was determined and the derived amino acid sequence reveals that the protein has 158 amino acid residues and a calculated molecular mass of 18,424 Da. Amino acid sequence comparison with the homologous counterparts from very diverse groups of organisms representing animals (human and rat), fungi (yeast) and plants (maize and Arabidopsis thaliana), shows that this protein is very conserved during evolution. Furthermore, ribosomal protein **S11** also shares a significant sequence homology to a set of related proteins: plastid ribosomal protein CS17 from different plants, Escherichia coli ribosomal protein S17 and Halobacterium marismortui ribosomal protein S14. (C) 1994 Academic Press, Inc.

L13 ANSWER 63 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1994:526442 CAPLUS
DN 121:126442
TI The **S11** and S13 self incompatibility alleles in Solanum chacoense Bitt. are remarkably similar
AU Saba-El-Leil, Marc K.; Rivard, Sylvain; Morse, David; Cappadocia, Mario
CS Inst. Rech. Biol. Veg., Quebec, H1X 2B2, Can.
SO Plant Mol. Biol. (1994), 24(4), 571-83
CODEN: PMBIDB; ISSN: 0167-4412
DT Journal
LA English
AB A genomic clone of the **S11** allele from the self-incompatibility locus (S locus) in Solanum chacoense Bitt. has been isolated by cross-hybridization to the S. chacoense S13 allele and sequenced. The sequence of the **S11** allele contains all the features expected for S genes of the Solanaceae, and **S11** expression, as assessed by northern blots and RNA-PCR, was similar to that of other S. chacoense S alleles. The **S11** protein sequence shares 95% identity with the phenotypically distinct S13 protein of S. chacoense and is the gametophytic S allele with the highest similarity to an existing allele so far discovered. Only 10 amino acid changes differentiate the mature proteins from these two alleles, which sets a new lower limit to the no.

of changes that can produce an altered S allele specificity. The amino acid substitutions are not clustered, suggesting that an accumulation of random point mutations can generate S allele diversity. The **S11** intron is unusual in that it could be translated in frame with the coding sequence, thus suggesting an addnl. mechanism for the generation of new S alleles.

L13 ANSWER 64 OF 122 SCISEARCH COPYRIGHT 2000 ISI (R)
AN 94:332795 SCISEARCH
GA The Genuine Article (R) Number: NM107
TI REDUCED DOSAGE OF GENES ENCODING RIBOSOMAL-PROTEIN S18 SUPPRESSES A MITOCHONDRIAL INITIATION CODON MUTATION IN SACCHAROMYCES-CEREVISIAE
AU FOLLEY L S (Reprint); FOX T D
CS CORNELL UNIV, GENET & DEV SECT, ITHACA, NY, 14853 (Reprint)
CYA USA
SO GENETICS, (JUN 1994) Vol. 137, No. 2, pp. 369-379.
ISSN: 0016-6731.
DT Article; Journal
FS LIFE; AGRI
LA ENGLISH
REC Reference Count: 80
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS
AB A yeast mitochondrial translation initiation codon mutation affecting the gene for cytochrome oxidase subunit III (COX3) was partially suppressed by a spontaneous nuclear mutation. The suppressor mutation also caused cold-sensitive fermentative growth on glucose medium. Suppression and cold sensitivity resulted from inactivation of the gene product of RPS18A, one of mio unlinked genes that code the essential cytoplasmic small subunit ribosomal protein termed S18 in yeast. The two S18 genes differ only by 21 silent substitutions in their exons; both are interrupted by a single intron after the 15th codon. Yeast S18 is homologous to the human **S11** (70% identical) and the Escherichia coli S17 (35% identical) ribosomal proteins. This highly conserved family of ribosomal proteins has been implicated in maintenance of translational accuracy and is essential for assembly of the small ribosomal subunit. Characterization of the original rps18a-1 missense mutant and rps18a Delta and rps18b Delta null mutants revealed that levels of suppression, cold sensitivity and paromomycin sensitivity all varied directly with a limitation of small ribosomal subunits. The rps18a-1 mutant was most affected, followed by rps18a Delta then rps18b Delta. Mitochondrial mutations that decreased COX3 expression without altering the initiation codon were not suppressed. This allele specificity implicates mitochondrial translation in the mechanism of suppression. We could not detect an epitope-tagged variant of S18 in mitochondria. Thus, it appears that suppression of the mitochondrial translation initiation defect is caused indirectly by reduced levels of cytoplasmic small ribosomal subunits, leading to changes in either cytoplasmic translational accuracy or the relative levels of cytoplasmic translation products.

L13 ANSWER 65 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1995:387193 CAPLUS
DN 123:7437
TI Mapping of serovar-specific monoclonal antibody epitopes by DNA and amino acid sequence analysis of Neisseria gonorrhoeae outer membrane protein IB strains
AU Chow, Vincent T. K.; Lau, Q. C.; Poh, C. L.
CS Faculty of Medicine, National University of Singapore, Singapore, 0511, Singapore
SO Immunol. Infect. Dis. (1994), 4(4), 202-6
CODEN: IINDEK; ISSN: 0959-4957
DT Journal
LA English
AB Recognition of ten Neisseria gonorrhoeae strains by serovar-specific

monoclonal antibodies (MAbs) was correlated with the complete **nucleotide** and deduced amino acid sequence of their resp. outer membrane protein IB (PIB). The sequences of 7 gonococcal strains (S7, S34, S22, S36, S386, **S11**, and S16) were obtained by PCR amplification and direct DNA sequencing, and were compared with the published sequences of 3 strains (P9, MS11, and R10). By identifying the differences in amino acid residues between strains which differ by 1 monoclonal antibody recognition, the corresponding putative epitopes were mapped. The epitope recognized by MAb 3C8 ('a') was mapped to codons 192-196 and 198, epitope 1F5 ('b') to codons 21, 22, 26, 27 and 35, epitope 2D6 ('c') to codons 238 and 240, epitope 2D4 ('h') to codons 236-238 and 240, and epitope 2H1 ('k') to around codons 201 and 202. These epitopes were proposed to occur within the predicted PIB surface-exposed loops 5 ('a' and 'k'), 1 ('b'), and 6 ('c' and 'h'). The localization of these epitopes by PCR and DNA sequencing may facilitate a better understanding of the epidemiol. and evolution of gonococcal PIB serovars, and their interaction with the host immune system.

L13 ANSWER 66 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1994:451010 CAPLUS
DN 121:51010
TI Complete sequence of the mitochondrial DNA of the Chlorophyte alga Prototheca wickerhamii. Gene content and genome organization
AU Wolff, Gabriele; Plante, Isabelle; Lang, B. Franz; Kueck, Ulrich; Burger, Gertraud
CS Ruhr-Univ. Bochum, Bochum, D-44780, Germany
SO J. Mol. Biol. (1994), 237(1), 75-86
CODEN: JMOBAK; ISSN: 0022-2836
DT Journal
LA English
AB The complete **nucleotide** sequence of the circular mitochondrial (mt) DNA of the chloropyte alga Prototheca wickerhamii has been detd. (55,328 base-pairs, A + T content 74.2%). The genes identified encode three subunits of the cytochrome oxidase, apocytochrome b, nine subunits of the NADH dehydrogenase complex (nad1 to 7, nad4L and nad9), three ATPase subunits (atp6, atp9, atp1 (also referred to as atpA)), three rRNAs (5 S (rrn5), small subunit (srn) and large subunit (lrn) RNA), 26 tRNAs, and 13 ribosomal proteins. A total of five group I introns reside in lrn and cox1, two of which include intronic open reading frames (ORFs). Five free-standing ORFs longer than 60 codons are present. Three of these ORFs are counterparts to genes encoding proteins of unknown function in plant mitochondria (orf25 and orfB of angiosperms and orf244 of liverwort), whereas two of them are unique. Mitochondrial genes are encoded on both DNA strands in a way that suggests the existence of two transcription units, each including approx. one half of the mitochondrial genome. The two intergenic regions in which transcription is believed to initiate and terminate are about ten times longer than the other intergenic regions (1118 and 1993 nt vs. 100 to 150 nt). A total of 29 recurring sequence motifs (30 to 200 nt long) have been found in intergenic regions. Nine different types of motifs are present, most of them arranged as tandem repeats. These motifs may be implicated in transcription, e.g. as signals for initiation, termination and/or processing. Phylogenetic anal. of the basis of the cox1 gene strongly suggested that P. wickerhamii and plant mitochondrial genomes are monophyletic. The finding of plant-specific mitochondrial genes such as orf25, orf244, orfB and rrn5 in P. wickerhamii mitochondria corroborates this idea.

L13 ANSWER 67 OF 122 SCISEARCH COPYRIGHT 2000 ISI (R)
AN 94:370660 SCISEARCH
GA The Genuine Article (R) Number: NQ858
TI IMMUNODETECTION OF RICE DWARF PHYTOREOVIRAL PROTEINS IN BOTH INSECT AND

PLANT HO[redacted]
AU SUZUKI N[redacted]eprint); SUGAWARA M; KUSANO T; [redacted]RI H; MATSUURA Y
CS AKITA PREFECTURAL COLL AGR, INST BIOTECHNOL, PLANT GENET ENGN LAB, OHGATA,
AKITA 01004, JAPAN (Reprint); KYOTO INST TECHNOL, DEPT APPL BIOL, SAKYO KU, KYOTO 606, JAPAN; NATL INST HLTH, DEPT VIROL 2, SHINJUKU KU, TOKYO 162, JAPAN
CYA JAPAN
SO VIROLOGY, (JUL 1994) Vol. 202, No. 1, pp. 41-48.
ISSN: 0042-6822.
DT Article; Journal
FS LIFE
LA ENGLISH
REC Reference Count: 42
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB Peptides encoded by truncated (S1 and S2) or full-length (S3 to **s11**) cDNAs of 11 of the 12 rice dwarf phytoreovirus (RDV) genome segments were expressed in a baculovirus vector system. Antibodies raised against each of the expressed peptides were used as probes to detect the authentic proteins encoded by the RDV open reading frame. Polypeptides identified as gene products of S1 to **S11** in both RDV-infected rice leaf and leafhopper (Nephotettix cincticeps) homogenates were the P1 minor core (170 kDa), P2 (130 kDa), P3 major core (110 kDa), Pns4 nonstructural (83 kDa), P5 (89 kDa), Pns6 nonstructural (56 kDa), P7 minor core (58 kDa), P8 outercapsid (43 kDa), Pns9 nonstructural (49 kDa), Pns10 nonstructural (35 kDa), end Pns11a nonstructural (23 kDa) proteins. These molecular masses were in accord with those obtained from previous in vitro translation analysis. The locations of P2 and P5 remain to be determined although both of these are assumed to be outer layer proteins. Quantitative detection showed that accumulation (per gram of total proteins) of the virus-coded proteins in rice leaves is much greater (more than 15 times) than that in leafhoppers and that the content of the individual proteins varies within a sample from rice or leafhopper and also varies among different samples. (C) 1994 Academic Press, Inc.

L13 ANSWER 68 OF 122 SCISEARCH COPYRIGHT 2000 ISI (R)DUPLICATE 12
AN 94:424996 SCISEARCH
GA The Genuine Article (R) Number: NV589
TI **NUCLEOTIDE**-SEQUENCE OF RICE DWARF PHYTOREOVIRUS GENOME SEGMENT-2 - COMPLETION OF SEQUENCE ANALYSES OF RICE DWARF VIRUS
AU UYEDA I (Reprint); SUDA N; YAMADA N; KUDO H; MURAO K; SUGA H; KIMURA I; SHIKATA E; KITAGAWA Y; KUSANO T; SUGAWARA M; SUZUKI N
CS HOKKAIDO UNIV, FAC AGR, DEPT AGROBIOL & BIORESOURCES, SAPPORO, HOKKAIDO 060, JAPAN (Reprint); AKITA PREFECTURAL COLL AGR, INST BIOTECHNOL, PLANT GENET ENGN LAB, OHGATA, JAPAN
CYA JAPAN
SO INTERVIROLOGY, (JAN/FEB 1994) Vol. 37, No. 1, pp. 6-11.
ISSN: 0300-5526.
DT Article; Journal
FS LIFE
LA ENGLISH
REC Reference Count: 38
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB The complete **nucleotide** sequence of rice dwarf phytoreovirus genome segment 2 (S2) was determined to be 3,512 **nucleotides** long with one open reading frame initiating at **nucleotide** 15 and terminating at **nucleotide** 3363. The encoded polypeptide was predicted to have 1,116 residues with a relative molecular weight of 123 kD. Comparison of S2 of two isolates showed they had identical lengths and 97 and 98.3% **nucleotide** and amino acid sequence identities,

respecti[illegible]y. A search of the Swiss-Prot data base (R 22.0) failed to fmd any prote[illegible]s with significant homology to the S2-encoded protein. Determination of the **nucleotide** sequence of the S2 has completed the sequence determination of the genome of rice dwarf virus. Homology searches made for proteins encoded by each of the genomic segments showed that the polypeptide encoded by **S11** has similarity to histone H1 protein and VP6 of blue tongue virus, indicating it might possess nucleic acid binding properties.

L13 ANSWER 69 OF 122 SCISEARCH COPYRIGHT 2000 ISI (R)DUPLICATE 13
AN 93:702769 SCISEARCH
GA The Genuine Article (R) Number: MG711
TI CLONING AND CHARACTERIZATION OF THE RNA-POLYMERASE ALPHA-SUBUNIT OPERON OF
CHLAMYDIA-TRACHOMATIS
AU TAN M; KLEIN R; GRANT R; GANEM D; ENGEL J (Reprint)
CS UNIV CALIF SAN FRANCISCO, DEPT MED, SAN FRANCISCO, CA, 94143; UNIV CALIF SAN FRANCISCO, DEPT MICROBIOL & IMMUNOL, SAN FRANCISCO, CA, 94143
CYA USA
SO JOURNAL OF BACTERIOLOGY, (NOV 1993) Vol. 175, No. 22, pp. 7150-7159.
ISSN: 0021-9193.
DT Article; Journal
FS LIFE
LA ENGLISH
REC Reference Count: 49
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS
AB We have cloned the chlamydial operon that encodes the initiation factor IF1, the ribosomal proteins L36, S13, and **S11**, and the alpha subunit of RNA polymerase. The genes for **S11** and alpha are closely linked in Escherichia coli, Bacillus subtilis, and plant chloroplast genomes, and this arrangement is conserved in Chlamydia spp. The **S11** ribosomal protein gene potentially encodes a protein of 125 amino acids with 41 to 42% identity over its entire length to its E. coli and B. subtilis homologs; the gene encoding the alpha subunit specifies a protein or 322 amino acids with 25 to 30% identity over its entire length to its E. coli and B. subtilis homologs. In a T7-based expression system in E. coli, the chlamydial alpha gene directed the synthesis of a 36-kDa protein. Mapping of the chlamydial mRNA transcript by RNase protection studies and by a combination of reverse transcription and the polymerase chain reaction demonstrates that IF1, L36, S13, **S11**, and alpha are transcribed as a polycistronic transcript.

L13 ANSWER 70 OF 122 SCISEARCH COPYRIGHT 2000 ISI (R)DUPLICATE 14
AN 93:393222 SCISEARCH
GA The Genuine Article (R) Number: LH124
TI IDENTIFICATION OF A REGION OF THE POLIOVIRUS GENOME INVOLVED IN PERSISTENT
INFECTION OF HEP-2 CELLS
AU CALVEZ V; PELLETIER I; BORZAKIAN S; COLBEREGARAPIN F (Reprint)
CS INST PASTEUR, UNITE VIROL MED, 25 RUE DR ROUX, F-75724 PARIS, FRANCE
CYA FRANCE
SO JOURNAL OF VIROLOGY, (JUL 1993) Vol. 67, No. 7, pp. 4432-4435.
ISSN: 0022-538X.
DT Note; Journal
FS LIFE
LA ENGLISH
REC Reference Count: 26
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS
AB Poliovirus mutants were selected during the persistent infection of human neuroblastoma cells. These viruses could establish secondary persistent infections in HEp-2 nonneural cells. We report the identification of a region of the genome of a persistent virus (**S11**) that was sufficient to confer to a recombinant virus the phenotype that causes persistent infection in HEp-2 cells. This region,

between **nucleotides** 1148 and 3481, contained 11 missense mutations mapping exclusively in the genes of capsid proteins VP1 and VP2.

Because recombinant viruses carrying only one of these two mutated genes were not able to cause persistent infection, it seems very probable that two or more mutations in these genes are required for expression of the phenotype that causes persistent infection.

L13 ANSWER 71 OF 122 SCISEARCH COPYRIGHT 2000 ISI (R)DUPLICATE 15
AN 93:245341 SCISEARCH
GA The Genuine Article (R) Number: KX335
TI PRECISE MISSENSE AND SILENT POINT MUTATIONS ARE FIXED IN THE GENOMES OF POLIOVIRUS MUTANTS FROM PERSISTENTLY INFECTED-CELLS
AU BORZAKIAN S; PELLETIER I; CALVEZ V; COLBEREGARAPIN F (Reprint)
CS INST PASTEUR, VIROL MED UNITE, 25 RUE DR ROUX, F-75724 PARIS, FRANCE
CYA FRANCE
SO JOURNAL OF VIROLOGY, (MAY 1993) Vol. 67, No. 5, pp. 2914-2917.
ISSN: 0022-538X.
DT Note; Journal
FS LIFE
LA ENGLISH
REC Reference Count: 37
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB Poliovirus mutants selected in persistently infected human neuroblastoma cells have a modified cell tropism and can establish a secondary persistent infection in nonneural cells, such as HEp-2c cells. **Nucleotide** sequence analysis revealed that the genome of a persistent mutant, **S11**, differed from that of the parental lytic Sabin 1 poliovirus strain by 31 point mutations. Three mutations occurred in the noncoding regions. The other mutations resulted in 12 amino acid substitutions; 1 substitution occurred in a nonstructural protein (3A), while the other 11 substitutions were clustered in the capsid proteins VP2 and VP1. The same missense mutations, as well as many of the silent mutations that we observed in mutant **S11**, also accumulated in the genome of two other persistent viruses isolated from independent infections. This finding indicates that both missense and silent mutations are selected during the persistent infection of neuroblastoma cells and suggests that the secondary structure of RNA in the coding region may play a role in viral infection.

L13 ANSWER 72 OF 122 SCISEARCH COPYRIGHT 2000 ISI (R)DUPLICATE 16
AN 93:367978 SCISEARCH
GA The Genuine Article (R) Number: LF503
TI IDENTIFICATION OF A DROSOPHILA PROTEIN SIMILAR TO RAT S13 AND ARCHAEBACTERIAL-**S11** RIBOSOMAL-PROTEINS
AU MCNABB S L (Reprint); ASHBURNER M
CS UNIV CAMBRIDGE, DEPT GENET, CAMBRIDGE CB2 3EH, ENGLAND
CYA ENGLAND
SO NUCLEIC ACIDS RESEARCH, (25 MAY 1993) Vol. 21, No. 10, pp. 2523.
ISSN: 0305-1048.
DT Note; Journal
FS LIFE
LA ENGLISH
REC Reference Count: 10

L13 ANSWER 73 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1993:576158 CAPLUS
DN 119:176158
TI A cDNA for Arabidopsis cytosol ribosomal protein **S11**
AU Lu, Guihua; Wu, Ke; Ferl, Robert J.
CS Hortic. Sci. Dep., Univ. Florida, Gainesville, FL, 32611, USA
SO Plant Physiol. (1993), 102(2), 695-6

CODEN: PI[redacted]AY; ISSN: 0032-0889
DT Journal
LA English
AB During an oligonucleotide screening for DNA binding proteins, pos. clones were isolated from a .lambda.gt11 cDNA expression library com. prepd. (Clontech) from Arabidopsis suspension-cell poly(A)+ RNA. One cDNA clone, designed as AT **S11**.beta., is 696 **nucleotides** long with an open reading frame extending from position 74 to 551. The first ATG triplet at position 74 is situated in this open reading frame, and the sequence around it (TAGCCATGGCT) shows homol. to the conserved sequence around plant initiation codons (TAACAATGGCT). A 12-**nucleotide** poly(A) tail is located at the 3' end. These facts suggest that the cDNA clone is a full-length clone encoding a polypeptide of 159 amino acids. Sequence comparison to the GenBank data base revealed no similarity to any DNA binding protein. Interestingly, homol. was found with cytosol ribosomal protein **S11** from Arabidopsis (92%), maize (84%), and human (54%). Although the deduced amino acid sequence of At **S11** .beta. has 92% similarity with a previously reported Arabidopsis cytosol ribosomal protein **S11** (At **S11**), the two cDNAs are distinct at the DNA sequence level. The present cDNA is referred to as At **S11**.beta. to distinguish it from the previous clone. It is concluded that there are at least two different genes encoding cytosol ribosomal protein **S11** in Arabidopsis thaliana.

L13 ANSWER 74 OF 122 SCISEARCH COPYRIGHT 2000 ISI (R)DUPLICATE 17
AN 93:95450 SCISEARCH
GA The Genuine Article (R) Number: KL717
TI TOPOGRAPHY OF THE E-SITE ON THE ESCHERICHIA-COLI RIBOSOME
AU WOWER J; SCHEFFER P; SYLVERS L A; WINTERMEYER W; ZIMMERMANN R A (Reprint)
CS UNIV MASSACHUSETTS, DEPT BIOCHEM & MOLEC BIOL, AMHERST, MA, 01003; UNIV WITTEN HERDECKE, INST MOLEK BIOL, W-5810 WITTEN, GERMANY; UNIV MASSACHUSETTS, PROGRAM MOLEC & CELLULAR BIOL, AMHERST, MA, 01003
CYA USA; GERMANY
SO EMBO JOURNAL, (FEB 1993) Vol. 12, No. 2, pp. 617-623.
ISSN: 0261-4189.
DT Article; Journal
FS LIFE
LA ENGLISH
REC Reference Count: 47
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS
AB Three photoreactive tRNA probes have been utilized in order to identify ribosomal components that are in contact with the aminoacyl acceptor end and the anticodon loop of tRNA bound to the E site of Escherichia coli ribosomes. Two of the probes were derivatives of E.coli tRNA(Phe) in which adenosines at positions 73 and 76 were replaced by 2-azidoadenosine. The third probe was derived from yeast tRNA(Phe) by substituting wyosine at position 37 with 2-azidoadenosine. Despite the modifications, all of the photoreactive tRNA species were able to bind to the E site of E.coli ribosomes programmed with poly(A) and, upon irradiation, formed covalent adducts with the ribosomal subunits. The tRNA(Phe) probes modified at or near the 3' terminus exclusively labeled protein L33 in the 50S subunit. The tRNA(Phe) derivative containing 2-azidoadenosine within the anticodon loop became cross-linked to protein **S11** as well as to a segment of the 16S rRNA encompassing the 3'-terminal 30 **nucleotides**. We have located the two extremities of the E site-bound tRNA on the ribosomal subunits according to the positions of L33, **S11** and the 3' end of 16S rRNA defined by immune electron microscopy. Our results demonstrate conclusively that the E site is topographically distinct from either the P

site or t[redacted]A site, and that it is located alongside the P site as expected for the tRNA exit site.

L13 ANSWER 75 OF 122 SCISEARCH COPYRIGHT 2000 ISI (R)DUPLICATE 18
AN 93:195329 SCISEARCH
GA The Genuine Article (R) Number: KU715
TI CLONING AND CHARACTERIZATION OF DIFFERENTIALLY EXPRESSED GENES FROM INVITRO-GROWN AMASTIGOTES OF LEISHMANIA-DONOVANI
AU JOSHI M; DWYER D M; NAKHASI H L (Reprint)
CS CBER, FOOD & DRUG ADM, DIV BIOCHEM & BIOPHYS, BIOCHEM LAB, BLDG 29, RM 107, 8800 ROCKVILLE PIKE, BETHESDA, MD, 20892; NIAID, PARASIT DIS LAB, BETHESDA, MD, 20892
CYA USA
SO MOLECULAR AND BIOCHEMICAL PARASITOLOGY, (APR 1993) Vol. 58, No. 2, pp. 345-354.
ISSN: 0166-6851.
DT Article; Journal
FS LIFE
LA ENGLISH
REC Reference Count: 30
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB Leishmanial parasites routinely undergo cyclic differentiation from promastigotes to amastigotes during their life cycle. This process involves both morphological and macromolecular changes. To study such changes, we used a axenic culture system which permits the continuous generation and cycling of Leishmania donovani from promastigotes to 'amastigotes' in vitro. cDNA libraries were constructed from poly(A)+ RNA isolated from both the pro- and amastigote forms. Using differential cDNA hybridization techniques, 3 unique cDNAs clones (P17, A41 and A45) were isolated from the amastigote library. To assess whether these clones were differentially expressed by the pro-or 'amastigotes' forms, they were hybridized to RNA isolated from each of these parasite forms in Northern and slot-blots. Results of these analyses showed that 'amastigotes' had approx. 2-fold higher levels of the A41 and A45 RNAs compared to the promastigotes. Conversely, promastigotes showed approx. 2-fold higher levels of the P17 RNA than 'amastigotes'. **Nucleotide** sequence analysis and comparison with those in Gene bank, revealed that the 3 cDNAs represent unique leishmanial genes. Comparison of the deduced amino acid sequences revealed that: P17 open reading frame (ORF) had significant similarity with a soybean ribosomal protein **S11**; A41 ORF with a Bacillus subtilis spore germination gene (gerC) and A45 ORF with yeast stress-inducible protein (STI1). It is of interest to note that. of the 3 cDNAs identified, the A45-encoded protein was recognized by sera from patients with clinically active visceral leishmaniasis and was encoded by a single copy gene.

L13 ANSWER 76 OF 122 SCISEARCH COPYRIGHT 2000 ISI (R)DUPLICATE 19
AN 93:539633 SCISEARCH
GA The Genuine Article (R) Number: LV200
TI POLYMERASE CHAIN-REACTION AND DIRECT SEQUENCING OF NEISSERIA-GONORRHOEAE PROTEIN-IB GENE - PARTIAL **NUCLEOTIDE** AND AMINO-ACID-SEQUENCE ANALYSIS OF STRAIN-S4, STRAIN-**S11**, STRAIN-S48 (SEROVAR-IB4) AND STRAIN-S-34 (SEROVAR-IB5)
AU LAU Q C; CHOW V T K (Reprint); POH C L
CS NATL UNIV SINGAPORE, FAC MED, DEPT MICROBIOL, KENT RIDGE, SINGAPORE 0511, SINGAPORE
CYA SINGAPORE
SO MEDICAL MICROBIOLOGY AND IMMUNOLOGY, (JUL 1993) Vol. 182, No. 3, pp. 137-145.
ISSN: 0300-8584.
DT Article; Journal
FS LIFE
LA ENGLISH
REC Reference Count: 11

ABSTRACTS AVAILABLE IN THE ALL AND IALL FORMATS

AB A pair of primers were designed for the polymerase chain reaction (PCR) to amplify a 341-base pair fragment of the gene encoding the outer membrane protein IB (PIB) of Neisseria gonorrhoeae. This PCR technique is specific and sensitive, being able to detect gonococcal strains belonging to ten different PIB serovars, but not PIA gonococcus nor other negative control bacteria. PCR products of four representative PIB strains were directly sequenced. Of the three strains belonging to serovar IB4, two (**S11** and S48) shared identical **nucleotide** and amino acid sequences in the PIB region examined. The third IB4 strain (S4) revealed sequences identical to the published IB26 strain (P9). The sequences of strains P9, S4, **S11** and S48 were found to differ from those of strain S34 (serovar IB5). The PCR sequencing technique can further differentiate strains belonging to a common serovar and establish clonal relationships among strains. As a molecular epidemiological tool, the PCR-sequencing strategy can augment existing typing methods including serotyping.

L13 ANSWER 77 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1993:248731 CAPLUS
DN 118:248731
TI The .alpha.-operon equivalent genome region in the extreme halophilic archaebacterium Haloarcula (Halobacterium) marismortui
AU Scholzen, Thomas; Arndt, Evelyn
CS Abt. Wittmann, Max-Planck-Inst. Mol. Gene., Berlin, W-1000, Germany
SO J. Biol. Chem. (1992), 267(17), 12123-30
CODEN: JBCHA3; ISSN: 0021-9258
DT Journal
LA English
AB The genome region of the extreme halophilic archaebacterium Haloarcula marismortui equiv. to the .alpha.-operon of Eschrichia coli has been characterized. In H. marismortui, the .alpha.-operon was located immediately upstream from the S9 gene cluster. The gene order in the halobacterial .alpha.-operon, given according to the gene products, is tRNASer, HmaS13, HmaS4, HmaS11, and HmaRp.alpha.. Compared to the corresponding operon from E. coli, the halobacterial gene organization differs in (1) the presence of a gene for tRNASer (GCU), (2) the reversed order of the genes for the ribosomal proteins HmaS11 and HmaS4, and (3) the absence of the gene coding for the ribosomal protein L17. The primary structure of HmaRp.alpha. shows high similarity to a subunit of eukaryotic RNA polymerase II (YeaRpB3, HsaRpB33), whereas the similarity to the eubacterial .alpha.-subunit of RNA polymerase is only weak.

L13 ANSWER 78 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1993:464442 CAPLUS
DN 119:64442
TI Function and evolution of a minimal plastid genome from a nonphotosynthetic parasitic plant
AU Wolfe, Kenneth H.; Morden, Clifford W.; Palmer, Jeffrey D.
CS Dep. Biol., Indiana Univ., Bloomington, IN, 47405, USA
SO Proc. Natl. Acad. Sci. U. S. A. (1992), 89(22), 10648-52
CODEN: PNASA6; ISSN: 0027-8424
DT Journal
LA English
AB Complete **nucleotide** sequencing shows that the plastid genome of Epifagus virginiana, a nonphotosynthetic parasitic flowering plant, lacks all genes for photosynthesis and chlororespiration found in chloroplast genomes of green plants. The 70,028-base-pair genome contains only 42 genes, at least 38 of which specify components of the gene-expression app. of the plastid. Moreover, all chloroplast-encoded RNA polymerase genes and many tRNA and ribosomal protein genes have been lost. Since the

genome is functional, nuclear gene products must compensate for some gene losses by means of previously unsuspected transport mechanisms that may operate in all plastids. At least one of the four unassigned protein genes in Epifagus plastid DNA must have a nongenetic and nonbioenergetic function and, thereby, serve as the reason for the maintenance of an active genome. Many small insertions in the Epifagus plastid genome create tandem duplications and presumably arose by slippage mispairing during DNA replication. The extensive redn. in genome size in Epifagus reflects an intensification of the same processes of length mutation that govern the amt. of noncoding DNA in chloroplast genomes. Remarkably, this massive pruning occurred with a virtual absence of gene order change.

L13 ANSWER 79 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1993:248805 CAPLUS
DN 118:248805
TI **Nucleotide** sequence of trnI(CAU) and rpl23 from Arabidopsis thaliana chloroplast genome
AU Luschnig, C.; Schweizer, D.
CS Inst. Bot., Univ. Wien, Vienna, A-1030, Austria
SO Nucleic Acids Res. (1992), 20(13), 3511
CODEN: NARHAD; ISSN: 0305-1048
DT Journal
LA English
AB This report describes the **nucleotide** sequences of trnI(CAU) and rpl23 of Arabidopsis thaliana chloroplast DNA. In higher plant chloroplast genomes, rpl23 has been described as part of a cluster of ribosomal proteins (L23-L2-S19-L22-S3-L16-L14-S8-L36-**S11**) which is located at the junction of the large single copy region (LSC) and the Inverted Repeat B (IRB). A part of this cluster, including rpl23 and rpl2, is duplicated in the Inverted Repeat A (IRA). Anal. of the isolated EMBL3-.lambda.-clone revealed that the sequence is part of the ribosomal protein cluster located at the border of LSC and IRB. The deduced protein has a mol. wt. of 10,793 and is almost identical with its tobacco and maize counterparts and shows high homol. to rpl23 from Marchantia polymorpha. The tRNAIle gene is located proximal to the rp-cluster and possesses a Met-Anticodon (CAU). It has 100% homol. to trnI of tobacco and spinach and also high similarity to its counterparts in rice and in Marchantia polymorpha.

L13 ANSWER 80 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1993:95360 CAPLUS
DN 118:95360
TI Gene clusters for ribosomal proteins in the mitochondrial genome of a liverwort, Marchantia polymorpha
AU Takemura, Miho; Oda, Kenji; Yamato, katsuyuki; Ohta, Eiji; Nakamura, Yasukazu; Nozato, Naoko; Akashi, Kinya; Ohyama, Kanji
CS Fac. Agric., Kyoto Univ., Kyoto, 606-01, Japan
SO Nucleic Acids Res. (1992), 20(12), 3199-205
CODEN: NARHAD; ISSN: 0305-1048
DT Journal
LA English
AB Sixteen genes for ribosomal proteins were detected in the complete sequence of the mitochondrial DNA from a liverwort, M. polymorpha. The genes formed two major clusters, rps12-rps7 and rps10-rpl2-rps19-rps3-rpl16-rpl5-rps14-rps8-rpl6-rps13-rps11-rps1, very similar in organization to Escherichia coli ribosomal protein operons (str and S10-spc-.alpha. operons, resp.). In contrast, rps2 and rps4 genes were located sep. in the liverwort mitochondrial genome (the latter was part of the .alpha. operon in E. coli). Furthermore, several ribosomal proteins encoded by the liverwort mitochondrial genome differed substantially in size from their counterparts in E. coli and liverwort chloroplast.

L13 ANSWER 8[illegible] OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1993:487[illegible] CAPLUS
DN 119:87653
TI Rapid evolution of the plastid translational apparatus in a nonphotosynthetic plant: loss or accelerated sequence evolution of tRNA and ribosomal protein genes
AU Wolfe, Kenneth H.; Morden, Clifford W.; Ems, Stephanie C.; Palmer, Jeffrey D.
CS Dep. Biol., Indiana Univ., Bloomington, IN, 47405, USA
SO J. Mol. Evol. (1992), 35(4), 304-17
CODEN: JMEVAU; ISSN: 0022-2844
DT Journal
LA English
AB The vestigial plastid genome of Epifagus virginiana (beechdrops), a nonphotosynthetic parasitic flowering plant, is functional but lacks 6 ribosomal protein and 13 tRNA genes found in the chloroplast DNAs of photosynthetic flowering plants. Import of nuclear gene products is hypothesized to compensate for many of these losses. Codon usage and amino acid usage patterns in Epifagus plastidic genes were not affected by the tRNA gene losses, though a small shift in the base compn. of the whole genome (toward A + T richness) is apparent. The ribosomal protein and tRNA genes that remain have had a high rate of mol. evolution, perhaps due to relaxation of constraints on the translational app. Despite the compactness and extensive gene loss, one translational gene (infA, encoding initiation factor 1) that is a pseudogene in tobacco has been maintained intact in Epifagus.

L13 ANSWER 82 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1993:33652 CAPLUS
DN 118:33652
TI Large scale cDNA sequencing for analysis of quantitative and qualitative aspects of gene expression
AU Okubo, Kousaku; Hori, Naohiro; Matoba, Ryo; Niiyama, Toshiyuki; Fukushima, Atsushi; Kojima, Yuko; Matsubara, Kenichi
CS Inst. Mol. Cell. Biol., Osaka Univ., Suita, 565, Japan
SO Nat. Genet. (1992), 2(3), 173-9
CODEN: NGENEC; ISSN: 1061-4036
DT Journal
LA English
AB Large scale sequencing of cDNAs provides a complementary approach to structural anal. of the human genome by generating expressed sequence tags (ESTs). Large-scale sequencing was undertaken of a 3'-directed cDNA library from the human liver cell line HepG2, that is a non-biased representation of the mRNA population. 982 Random cDNA clones were sequenced yielding more than 270 kilobases. A significant portion of the identified genes encoded secretable proteins and components for protein-synthesis. The abundance of cDNA species varied from 2.2% to <0.004%. Fifty-two percent of the mRNA were abundant species consisting of 173 genes and the rest were non-abundant, consisting of .apprx.6600 genes.

L13 ANSWER 83 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1993:206510 CAPLUS
DN 118:206510
TI Complete **nucleotide** sequence of the mitochondrial DNA from a liverwort, Marchantia polymorpha
AU Oda, Kenji; Yamato, Katsuyuki; Ohta, Eiji; Nakamura, Yasukazu; Takemura, Miho; Nozato, Naoko; Akashi, Kinya; Kanegae, Takeshi; Ogura, Yutaka; et al.

CS Fac. Agri[redacted] Kyoto Univ., Kyoto, 606-01, Japan
SO Plant Mol[redacted]Biol. Rep. (1992), 10(2), 105-6[redacted]
CODEN: PMBRD4; ISSN: 0735-9640
DT Journal
LA English
AB Libraries of cosmid and plasmid clones covering the entire region of mitochondrial DNA from the liverwort M. polymorpha were constructed. These clones were used for the detn. of the complete **nucleotide** sequence of the liverwort mitochondrial DNA (total of 186,608 base pairs) and including genes for 3 species of rRNAs, 29 genes for 27 species of tRNAs, and 30 genes for functionally known proteins (16 ribosomal proteins, 3 subunits of cytochrome c oxidase, apocytochrome b protein, 3 subunits of H+-ATPase, and 7 subunits of NADH-ubiquinone oxidoreductase). The genome also contains 32 unidentified open reading frames. Thus, the complete **nucleotide** sequences from both chloroplast and mitochondrial genomes have been detd. in the same organism.

L13 ANSWER 84 OF 122 SCISEARCH COPYRIGHT 2000 ISI (R)DUPLICATE 20
AN 92:56601 SCISEARCH
GA The Genuine Article (R) Number: GZ517
TI PLASTID DNA FROM PYRENOMONAS-SALINA (CRYPTOPHYCEAE) - PHYSICAL MAP, GENES,
AND EVOLUTIONARY IMPLICATIONS
AU MAERZ M (Reprint); WOLTERS J; HOFMANN C J B; SITTE P; MAIER U G
CS INST BIOL 2, LEHRSTUHL ZELLBIOL, SCHANZLESTR 1, W-7800 FREIBURG, GERMANY (Reprint); UNIV KIEL, INST ALLGEMEINE MIKROBIOL, W-2300 KIEL 1, GERMANY
CYA GERMANY
SO CURRENT GENETICS, (JAN 1992) Vol. 21, No. 1, pp. 73-81.
ISSN: 0172-8083.
DT Article; Journal
FS LIFE
LA ENGLISH
REC Reference Count: 66
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS
AB Cryptomonads are thought to have arisen from a symbiotic association between a eukaryotic flagellated host and a eukaryotic algal symbiont, presumably related to red algae. As organellar DNAs have proven to be useful tools in elucidating phylogenetic relationships, the plastid (pt) DNA of the cryptomonad alga Pyrenomonas salina has been characterized in some detail. A restriction map of the circular 127 kb ptDNA from Pyrenomonas salina was established. An inverted repeat (IR) region of about 5 kb separates two single-copy regions of 15 and 102 kb, respectively. It contains the genes for the small and large subunit of rRNA. Ten protein genes, coding for the large subunit of ribulose-1,5-bisphosphate carboxylase, the 47 kDa, 43 kDa and 32 kDa proteins of photosystem II, the ribosomal proteins L2, S7 and **S11** , the elongation factor Tu, as well as the alpha- and beta-subunits of ATP
synthase, have been localized on the restriction map either by hybridization of heterologous gene probes or by sequence homologies. The gene for the plastidal small subunit (SSUr) RNA has been sequenced and compared to homologous SSU regions from the cyanobacterium Anacystis nidulans and plastids from rhodophytes, chromophytes, euglenoids, chlorophytes, and land plants. A phylogenetic tree constructed with the neighborliness method and indicating a relationship of cryptomonad plastids with those of red algae is presented.

L13 ANSWER 85 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1993:162020 CAPLUS
DN 118:162020
TI Buchnera aphidicola, the endosymbiont of aphids, contains genes for four ribosomal RNA proteins, initiation factor-3, and the .alpha.-subunit of RNA polymerase
AU Munson, Mark A.; Baumann, Linda; Baumann, Paul
CS Dep. Microbiol., Univ. California, Davis, CA, 95616-8665, USA

SO Curr. Mic[redacted]iol. (1992), 24(1), 23-9
CODEN: CU[redacted]D; ISSN: 0343-8651

DT Journal
LA English
AB B. aphidicola is a prokaryotic endosymbiont of the aphid Schizaphis graminum. With the polymerase chain reaction (PCR) and oligonucleotide primers to conserved regions, 2 DNA fragments of the endosymbiont .alpha.-operon and L20 operon were amplified, cloned into Escherichia coli, and their sequences were detd. The results indicated that the organization of the endosymbiont genes on these fragments was identical to that of the corresponding operons of E. coli. The 1032-base-pair (bp) fragment of the .alpha.-operon contained the genes for small ribosomal subunit proteins **S11** and S4, followed by the gene for the .alpha.-subunit of RNA polymerase (.alpha.-RNAP). The 702-bp fragment of the L20-operon contained the genes for initiation factor-3 (IF3) and large ribosomal subunit proteins L35 and L20. As in other prokaryotes, the genes of the .alpha.-operon and the L20-operon were present as single copies in the genome of B. aphidicola. Comparisons of the amino acid sequences of these proteins were consistent with the previously established close relationship between B. aphidicola and E. coli and a distant relationship to species of Bacillus.

L13 ANSWER 86 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1993:184615 CAPLUS
DN 118:184615
TI Gene organization deduced from the complete sequence of liverwort Marchantia polymorpha mitochondrial DNA. A primitive form of plant mitochondrial genome
AU Oda, Kenji; Yamato, Katsuyuki; Ohta, Eiji; Nakamura, Yasukazu; Takemura, Miho; Nozato, Naoko; Akashi, Kinya; Kanegae, Takeshi; Ogura, Yutaka; et al.
CS Fac. Agric., Kyoto Univ., Kyoto, 606, Japan
SO J. Mol. Biol. (1992), 223(1), 1-7
CODEN: JMOBAK; ISSN: 0022-2836
DT Journal
LA English
AB Anal. of the mitochondrial DNA of a liverwort M. polymorpha by electron microscopy and restriction endonuclease mapping indicated that the liverwort mitochondrial genome was a single circular mol. of .apprx.184,400 base-pairs. The complete sequence of the liverwort mitochondrial DNA was detd. and 94 possible genes were detected in the sequence of 186,608 base-pairs. These included genes for 3 species of rRNA, 29 genes for 27 species of tRNA, and 30 open reading frames (ORFs) for functionally known proteins (16 ribosomal proteins, 3 subunits of H+-ATPase, 3 subunits of cytochrome c oxidase, apocytochrome b protein, and 7 subunits of NADH-ubiquinone oxidoreductase). Three ORFs showed similarity to ORFs of unknown function in the mitochondrial genomes of other organisms. Furthermore, 29 ORFs were predicted as possible genes by using the index of G + C content in first, second and third letters of codons (42.0, 37.0, and 26.4%, resp.) obtained from the codon usages of identified liverwort genes. To date, 32 introns belonging to either group I or group II intron have been found in the coding regions of 17 genes including rRNA genes (rrn18 and rrn26), a tRNA gene (trnS) and a pseudogene (.psi.nad7). RNA editing was apparently lacking in liverwort mitochondria since the **nucleotide** sequences of the liverwort mitochondrial DNA were well-conserved at the DNA level.

L13 ANSWER 87 OF 122 SCISEARCH COPYRIGHT 2000 ISI (R)DUPLICATE 21
AN 91:628219 SCISEARCH
GA The Genuine Article (R) Number: GP521
TI **NUCLEOTIDE**-SEQUENCES OF GENOME SEGMENTS S8, ENCODING A CAPSID

PROTEIN, [redacted] S10, ENCODING A 36K PROTEIN, OF RICE GALL DWARF VIRUS
AU NODA H; [redacted]IKAWA K; HIBINO H; KATO H; OMU[redacted] (Reprint)
CS NATL INST SERICULTURAL & ENTOMOL SCI, TSUKUBA, IBARAKI 305, JAPAN; NATL AGR RES CTR, TSUKUBA, IBARAKI 305, JAPAN
CYA JAPAN
SO JOURNAL OF GENERAL VIROLOGY, (1991) Vol. 72, No. NOV, pp. 2837-2842.
DT Article; Journal
FS LIFE
LA ENGLISH
REC Reference Count: 28
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB The **nucleotide** sequences of DNAs complementary to the eighth (S8) and the tenth (S10) largest of the 12 genome segments of rice gall dwarf virus (RGDV) were determined. The S8 and S10 segments consist of 1578 and 1198 **nucleotides**, each with a single open reading frame extending for 1278 **nucleotides** from **nucleotide** 21, and 960 **nucleotides** from **nucleotide** 22, respectively. S8 encodes a polypeptide of 426 amino acids with an M(r) of 47419. The amino acid sequences of several peptide fragments of the major outer capsid protein reported as 45K were contained in the predicted polypeptide. This protein, renamed the 47K protein, showed high homology with the outer capsid proteins of rice dwarf virus (RDV) and wound tumour virus (WTV); there was 56, 52 and 48% amino acid sequence identity between RGDV and WTV, RGDV and RDV, and RDV and WTV, respectively. S10 had the coding potential for a polypeptide of 320 amino acids with an M(r) of 36095 (36K protein), which exhibits 32% and 35% amino acid sequence identity with the predicted translation product of RDV S9 and the P9 capsid protein encoded by WTV **S11**, respectively. The conserved terminal sequences 5' GG ... GAU 3' which are present in all genome segments of WTV and RDV so far analysed, and in S9 of RGDV, were also found in RGDV S8 and S10. This conserved sequence together with the segment-specific inverted repeats found in the terminal sequence of RGDV S8 and S10 are thus characteristic structures common to all three phytoreoviruses. The **nucleotide** sequence of the region surrounding the inverted repeats was more similar between RGDV and WTV than between RGDV and RDV.

L13 ANSWER 88 OF 122 SCISEARCH COPYRIGHT 2000 ISI (R)DUPLICATE 22
AN 91:519878 SCISEARCH
GA The Genuine Article (R) Number: GE992
TI MOLECULAR ANALYSIS OF RICE DWARF PHYTOREOVIRUS SEGMENT-**S11** CORRESPONDING TO WOUND TUMOR PHYTOREOVIRUS SEGMENT-S12
AU SUZUKI N (Reprint); HARADA M; KUSANO T
CS AKITA PREFECTURAL COLL AGR, INST BIOTECHNOL, PLANT GENET ENGN LAB, OHGATA, AKITA 01004, JAPAN (Reprint)
CYA JAPAN
SO JOURNAL OF GENERAL VIROLOGY, (1991) Vol. 72, No. SEP, pp. 2233-2237.
DT Article; Journal
FS LIFE
LA ENGLISH
REC Reference Count: 34
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB The complete **nucleotide** sequence of rice dwarf phytoreovirus (RDV) genome segment **S11** was determined. **S11** is 1067 **nucleotides** long. There is an inverted repeat of 10 bp adjacent to the conserved 5'-terminal hexanucleotide (5' GGUAAA 3') and 3'-terminal tetranucleotide (5' UAGU 3') sequences. A single large open reading frame found in the plus strand of **S11** begins with the first AUG codon (bases 6 to 8) and extends for 567 bases. Evolutionary relatedness

between [redacted] **S11** and wound tumour phytoreovirus S12 based on amino acid sequence similarity (25.8%) was found. In addition to the first AUG triplet, RDV **S11** possesses a second in-phase AUG triplet (positions 30 to 32) nearby, which conforms to the Kozak consensus sequence. Two forms of the protein were identified by using an in vitro transcription and translation system in which a tailored full-length cDNA was the initial template. The abolition of the first AUG codon by site-directed mutagenesis resulted in disappearance of the larger translation product. These results strongly suggest that the two products are translated from the first and second AUG codons. Whether the two proteins are expressed in vivo is at present unclear.

L13 ANSWER 89 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1992:646339 CAPLUS
DN 117:246339
TI First field isolation of wound tumor virus from a plant host: minimal sequence divergence from the type strain isolated from an insect vector
AU Hillman, Bradley I.; Anzola, John V.; Halpern, Barbara T.; Cavileer, Timothy D.; Nuss, Donald L.
CS Dep. Plant Pathol., Rutgers Univ., New Brunswick, NJ, 08903, USA
SO Virology (1991), 185(2), 896-900
CODEN: VIRLAX; ISSN: 0042-6822
DT Journal
LA English
AB A new strain of wound tumor virus (WTV) has been isolated from a periwinkle plant (Catharanthus roseus), that was among several used as bait plants in a blueberry field. The 12 segments of double-stranded RNA of the viral genome were isolated directly from infected tissue and found to have mobilities through agarose gels that were identical to those of the type strain WTV. Coupled cDNA (cDNA) and polymerase chain reactions (PCR) primed with oligonucleotides complementary to the termini of segments 4-12 of the type strain of WTV successfully amplified those segments. Amplification products of the 9 segments were of the size expected for the full-length segment, with no shorter than full-length products representing defective RNAs detected. PCR products representing segments 7, 11, and 12 were cloned and sequenced in their entirety. The sequence of each segment varied only slightly from the homologous segment of the type strain. Variation ranged from less than 1% for segment 12 to approx. 3% for segment 7, but even these low levels of variation were much greater than the variation found in WTV isolates maintained in the lab. Most of the variation in each of the three segments was confined to the coding regions, and most of the differences were third position transitions. The new WTV strain has been designated WTVNJ.

L13 ANSWER 90 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1991:507265 CAPLUS
DN 115:107265
TI Bluetongue virus evolution: sequence analyses of the genomic S1 segments and major core protein VP7
AU Kowalik, Timothy F.; Li, Joseph K. K.
CS Mol. Biol. Program, Utah State Univ., Logan, UT, 84322-5500, USA
SO Virology (1991), 181(2), 749-55
CODEN: VIRLAX; ISSN: 0042-6822
DT Journal
LA English
AB The S1 segments, encoding the group-specific antigen, VP7, from the five

United St[redacted]s prototype bluetongue virus (BTV) serotypes were cloned as full-leng[redacted] entities. The **nucleotide** and [redacted]uced amino acid sequences of segment S1 of BTV-2 were detd. and compared with BTV-10, -11, -13, and -17, completing the sequencing of this cognate gene segment from all five US BTV serotypes. Each segment is 1156 bp long and contains an open reading frame encoding the 349-amino acid VP7 protein. Most (>94%) of the amino acids of VP7 among the serotypes are conserved, including the location (position 255) of a single lysine residue. Secondary structure analyses of VP7 predict a putative eight-stranded .beta.-barrel between amino acid positions 150 and 250, a structure similar to that obsd. in ssRNA viruses. The S1 genes are flanked by conserved 5' and 3' noncoding regions. Stem-loop structures are predicted at the 3' end of each gene (**nucleotide** positions 1058-1097). The S1 segments of BTV-2, -10, -11, and -17 have >93% of the **nucleotides** conserved, while <80% of their bases are identical with BTV-13. Analyses of **nucleotide** mismatches in each codon position of the VP7 open reading frame, transition frequencies, and evolutionary distances show that of the five, BTV-13 is the most distantly related and that BTV-10 and -17 are the most closely related serotypes. Evolutionary distance calcns. of segment L2 from BTV-10, -11, and -17 concur with these observations. Comparison of this relationship with hybridization data of segment M3, which codes for VP5, suggests that BTV-17 has evolved by a combination of genetic drift and genomic reassortment. The data also indicate that the five US BTV serotypes are derived from two distinct gene pools. Evolution distances were used to est. an evolution rate of 2.2 .times. 10-3 **nucleotide** substitution/site/yr for BTV segment S1. This rate is similar to the genes of retroviruses and implies an absence of RNA polymerase proofreading activity for dsRNA viruses.

L13 ANSWER 91 OF 122 SCISEARCH COPYRIGHT 2000 ISI (R)DUPLICATE 23
AN 91:440724 SCISEARCH
GA The Genuine Article (R) Number: FZ502
TI **NUCLEOTIDE**-SEQUENCE AND CHARACTERIZATION OF A MAIZE CYTOPLASMIC RIBOSOMAL PROTEIN-**S11** CDNA
AU LEBRUN M (Reprint); FREYSSINET G
CS RHONE POULENC AGROCHIM, BIOL MOLEC & CELLULAIRE VEGETALE LAB, 14-20 RUE PIERRE BAIZET, F-69009 LYONS, FRANCE (Reprint)
CYA FRANCE
SO PLANT MOLECULAR BIOLOGY, (1991) Vol. 17, No. 2, pp. 265-268.
DT Note; Journal
FS LIFE; AGRI
LA ENGLISH
REC Reference Count: 7
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS
AB We isolated a Zea mays cDNA encoding the 40S subunit cytoplasmic ribosomal protein **S11**. The **nucleotide** sequence was determined and the derived amino acid sequence compared to the corresponding Arabidopsis thaliana protein showing an homology of 90%. This ribosomal protein is encoded by a small multigene family of at least two members. The mRNA steady-state level is about one order of magnitude higher in rapidly growing parts of the plant such as the roots and shoots of seedlings compared to fully expanded leaf tissue.

L13 ANSWER 92 OF 122 SCISEARCH COPYRIGHT 2000 ISI (R)DUPLICATE 24
AN 91:475265 SCISEARCH
GA The Genuine Article (R) Number: GB744
TI INTERCISTRONIC GROUP-III INTRONS IN POLYCISTRONIC RIBOSOMAL-PROTEIN OPERONS OF CHLOROPLASTS
AU STEVENSON J K; DRAGER R G; COPERTINO D W; CHRISTOPHER D A; JENKINS K P; YEPIZPLASCENCIA G; HALLICK R B (Reprint)
CS UNIV ARIZONA, DEPT MOLEC & CELLULAR BIOL, TUCSON, AZ, 85721; UNIV ARIZONA, DEPT BIOCHEM, TUCSON, AZ, 85721

CYA USA
SO MOLECULAR & GENERAL GENETICS, (1991) Vol. 228, No. 1-2, pp. 183-192.
DT Article; Journal
FS LIFE
LA ENGLISH
REC Reference Count: 48
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB A novel ribosomal protein operon in the Euglena gracilis chloroplast genome was characterized. It encodes the genes for ribosomal proteins S4 and **S11** (rps4 and rps11). The coding region of the rps11 gene is interrupted by two introns of 107 and 100 bp. The introns belong to a distinct class known as group III introns. The major transcript from this operon was characterized as a fully spliced dicistronic rps4-rps11 mRNA by RNA blot analysis, primer extension sequencing, and cDNA cloning and sequencing. An additional 95 **nucleotide** (nt) group III intron was identified in the 123 nt rps4-rps11 intercistronic region. The identification of the intercistronic intron between the rps4 and rps11 genes was unexpected. Other RNA transcripts from regions of the genome that could potentially contain intercistronic introns were re-examined and two other intercistronic, group III introns were found. These are located in a large ribosomal protein operon between the genes for the ribosomal proteins L23 and L2, and between L14 and L5. There are at least 50 group III introns in the E. gracilis chloroplast genome. All but 6 are found in genes encoding protein components of the transcriptional and translational apparatus. The distribution of group III introns and the unusual location of intercistronic group III introns may reflect some aspect of gene expression, or provide some insight into the mechanism of their splicing.

L13 ANSWER 93 OF 122 SCISEARCH COPYRIGHT 2000 ISI (R)
AN 91:87295 SCISEARCH
GA The Genuine Article (R) Number: EW764
TI RIBOSOMAL AND CHROMOSOMAL PROTEIN CDNA CLONES OF XENOPUS-LAEVIS THYMUS ISOLATED WITH DIFFERENTIAL SCREENING
AU GROSSBERGER D (Reprint); FLAJNIK M; MARCUZ A
CS BASEL INST IMMUNOL, CH-4005 BASEL, SWITZERLAND
CYA SWITZERLAND
SO COMPARATIVE BIOCHEMISTRY AND PHYSIOLOGY B-COMPARATIVE BIOCHEMISTRY, (1991)
Vol. 98, No. 1, pp. 127-133.
DT Article; Journal
FS LIFE
LA ENGLISH
REC Reference Count: 32
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB 1. Xenopus laevis is an excellent system for the study of the evolution and ontogeny of the immune system. But since only immunoglobulin genes have been isolated from this species, we undertook to isolate other genes expressed in an immunologically important organ, the thymus.
2. We used differential screening of a thymus cDNA library with cDNA probes made from thymus and from erythroblasts.
3. Approximately 50 clones which hybridized to the probe from thymus, but not from erythroblast, were isolated and sequenced from their termini.
4. Several clones were identified in data bank searches by their similarity to previously published sequences, and the partial sequences of

these loci are reported here.
5. These include elongation factor 2, ribosomal protein **S11**, ribosomal protein S13, and the high mobility group protein.
6. Although these genes are not expected to be involved in an immune function, the availability of these sequences will facilitate the study of these loci in this species.

L13 ANSWER 94 OF 122 SCISEARCH COPYRIGHT 2000 ISI (R)
AN 91:446667 SCISEARCH
GA The Genuine Article (R) Number: GA207
TI A TRANSIENT DECREASE IN N-MYC EXPRESSION AND ITS BIOLOGICAL ROLE DURING DIFFERENTIATION OF HUMAN EMBRYONAL CARCINOMA-CELLS
AU HASEGAWA T; HARA E; TAKEHANA K; NAKADA S; ODA K (Reprint); KAWATA M; KIMURA H; SEKIYA S
CS SCI UNIV TOKYO, DEPT BIOL SCI & TECHNOL, NODA, CHIBA 278, JAPAN; SCI UNIV TOKYO, DEPT APPL BIOL SCI, NODA, CHIBA 278, JAPAN; CHIBA UNIV, SCH MED, DEPT OBSTET & GYNECOL, CHIBA 280, JAPAN
CYA JAPAN
SO DIFFERENTIATION, (1991) Vol. 47, No. 2, pp. 107-117.
DT Article; Journal
FS LIFE
LA ENGLISH
REC Reference Count: 41
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS
AB The human embryonal carcinoma (EC) cell line, NEC14 can be induced to morphologically differentiate by the addition of 10(-2) M N,N'-hexamethylene-bis-acetamide (HMBA) in vitro. The expression of several cellular oncogenes (c-onc) in NEC14 cells was examined after induction of differentiation by HMBA. The level of N-myc expression was the highest in undifferentiated cells but decreased transiently to less than 1/10 of the original level shortly after the induction of differentiation. To investigate the role of the transient decrease in N-myc level on NEC14 cell differentiation, a chimeric human N-myc gene in which transcription is initiated at the human beta-actin gene promoter was constructed and introduced into NEC14 cells. Several transformants expressing the exogenous N-myc gene constitutively were established. These transformants showed 10- to 70-fold increases in plating efficiency and shorter population doubling times as compared with the parental NEC14 cells. The transformants were hard to induce, spontaneously differentiated cells on the periphery of cell clusters in culture, unlike parental NEC14 cells, and took longer for HMBA-induced morphological differentiation. The populations of the cells expressing HLA and SSEA-1 antigens increased from 10%-20% to nearly 100% in NEC14 cells after the induction of differentiation, while the populations expressing these antigensincreased only to 50%-60% in one of the transformants, **S11** . The transformants gained an increased tumorigenic potential in nude mice, and the tumors produced consisted exclusively of EC stem cells. These results suggest that the additional expression of the exogenous N-myc gene (increased about two-fold) confers the more transformed state on the cells.

L13 ANSWER 95 OF 122 SCISEARCH COPYRIGHT 2000 ISI (R)
AN 91:9920 SCISEARCH
GA The Genuine Article (R) Number: EP140
TI LOCALIZATION OF A SERIES OF RNA-PROTEIN CROSS-LINK SITES IN THE 23S AND 5S RIBOSOMAL-RNA FROM ESCHERICHIA-COLI, INDUCED BY TREATMENT OF 50S SUBUNITS WITH 3 DIFFERENT BIFUNCTIONAL REAGENTS.
AU OSSWALD M; GREUER B; BRIMACOMBE R (Reprint)
CS MAX PLANCK INST MOLEC GENET, WITTMANN ABT, W-1000 BERLIN 33, GERMANY
CYA GERMANY
SO NUCLEIC ACIDS RESEARCH, (1990) Vol. 18, No. 23, pp. 6755-6760.
DT Article; Journal

FS LIFE
LA ENGLISH
REC Reference Count: 29
ABSTRACT IS AVAILABLE IN THE ALL AND. IALL FORMATS

AB 50S ribosomal subunits were reacted with bis-(2-chloroethyl)methylamine, 2-iminothiolane or methyl p-azidophenyl acetimidate, and RNA-protein cross-link sites on the RNA were localised using our published procedures. The degree of precision with which these sites could be determined was variable, depending on the particular protein or RNA region concerned. The following positions in the 23S RNA were identified as following positions in the 23S RNA were identified as encompassing the individual cross-link sites (numbered from the 5'-end, with asterisks denoting sites previously reported): L1, 1864-67, 1876-78,2119-33, 2163-72*; L2, 1819-20*; L3, 2832-34; L4, 320-25*; 613-17*; L5, 2307; L6, 2473-81*; L9, 1484-91; L11, 1060-62; L13, 547-50; L14, 1993-2002; L17, 1260-95; L18, 2307-20; L19, 1741-58; L21, 544-48*; 1198-1248; L23, 63-65, 137-41*; L24, 99-107*; L27, 2272-83, 2320-23*; 2332-37*; L28, 195-242, 368-424; L29, 101-02*; L30, 931-38; L32, 2878-90; L33, 2422-234. Crosslinks to 5S RNA were observed with L5 (positions 34-41), and L18 (precise site not localised).

L13 ANSWER 96 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1990:625457 CAPLUS
DN 113:225457
TI **Nucleotide** sequence and map positions of the duplicated gene for maize (Zea mays) chloroplast ribosomal protein L2
AU Kavousi, Mehdi; Giese, Klaus; Larrinua, Ignacio M.; McLaughlin, William E.; Subramanian, Alap R.
CS Abt. Wittmann, Max-Planck-Inst. Mol. Genet., Berlin, D-1000/33, Fed. Rep. Ger.
SO Nucleic Acids Res. (1990), 18(14), 4244
CODEN: NARHAD; ISSN: 0305-1048
DT Journal
LA English
AB The **nucleotide** sequence of 1797 bp in the inverted repeat (IR) of maize chloroplast DNA encoding ribosomal protein L2, tRNAHis, and flanking regions are reported. This data completes the sequence of the large r-protein gene cluster (L23-L2-S19-L22-S3-L16-L14-S8-L36-**S11**) in the maize chloroplast. The rpl2 gene contains a 564 bp intron of group II. The exons encode a basic protein (net charge +42) of 273 residues, Mr 30,174. The deduced amino acid sequence is 97, 89, 68, 54, and 44% identical to the homologous sequences in rice, tobacco, liverwort, Bacillus stearothermophilus, and Escherichia coli+, resp. As in rice, maize rpl2 has the unusual start codon ACG. Whether this putative initiation codon is functional is under investigation. Evidence for rpl2 expression, and N-terminal methylation of the protein has been derived from protein sequencing.

L13 ANSWER 97 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1990:419633 CAPLUS
DN 113:19633
TI Plant cytosolic ribosomal protein **S11** and chloroplast ribosomal protein CS17. Their primary structures and evolutionary relationships
AU Gantt, J. Stephen; Thompson, Michael D.
CS Plant Mol. Genet. Inst., Univ. Minnesota, St. Paul, MN, 55108, USA
SO J. Biol. Chem. (1990), 265(5), 2763-7
CODEN: JBCHA3; ISSN: 0021-9258
DT Journal
LA English
AB CDNA clones specific for Arabidopsis thaliana cytosolic ribosomal protein **S11** and plastid ribosomal protein CS17, both of which are encoded in the nuclear genome, have been isolated through the use of the corresponding soybean and pea cDNAs as probes, resp. The **nucleotide** sequences of all 4 cDNAs were detd. The amino acids

sequences derived from these cDNA sequences show that the soybean and A. thaliana CS1 cDNAs encode proteins that are homologous to rat ribosomal protein **S11** and that the pea and A. thaliana CS17 cDNAs encode proteins that are homologous to Escherichia coli ribosomal protein S17. The plant **S11** cytosolic ribosomal proteins also show significant sequence similarity to both E. coli ribosomal protein S17 and plastid CS17 indicating that these are all related proteins. Comparison of A. thaliana CS1 with A. thaliana **S11** and with E. coli S17 suggests that CS17 is more related to S17 than it is to **S11**. These results support the idea that the gene encoding CS17 was derived from a prokaryotic endosymbiont and not from a duplication of the eukaryotic **S11** gene.

L13 ANSWER 98 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1990:194139 CAPLUS
DN 112:194139
TI DNA-hybridization electron microscopy. Tertiary structure of 16 S rRNA
AU Oakes, Melanie I.; Kahan, Lawrence; Lake, James A.
CS Mol. Biol. Inst., Univ. California, Los Angeles, CA, 90024, USA
SO J. Mol. Biol. (1990), 211(4), 907-18
CODEN: JMOBAK; ISSN: 0022-2836
DT Journal
LA English
AB Seven regions of 16 S rRNA located on the surface of the 30 S ribosomal subunit, in a model for the tertiary structure of 16 S rRNA, account for .apprx.40% of the total 16 S rRNA. A structure labeled the platform ring is proposed for a region of rRNA within the central domain. This structure rings the edges of the platform and includes regions 655-751 and 769-810. Another region, the recognition complex, consists of **nucleotides** 500-545, and occupies a region on the exterior surface of the subunit near the elongation factor Tu-binding site. Ribosomal proteins mapped by immunoelectron microscopy are superimposed into the model to examine possible regions of interaction. Good correlation between the model locations of ribosomal proteins, and regions of rRNA protected by ribosomal proteins provide independent support for this model.

L13 ANSWER 99 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1991:57667 CAPLUS
DN 114:57667
TI The primary structure of rat ribosomal protein S13
AU Suzuki, Katsuyuki; Olvera, Joe; Wool, Ira G.
CS Dep. Biochem. Mol. Biol., Univ. Chicago, Chicago, IL, 60637, USA
SO Biochem. Biophys. Res. Commun. (1990), 171(2), 519-24
CODEN: BBRCA9; ISSN: 0006-291X
DT Journal
LA English
AB The covalent structure of the rat 40 S ribosomal subunit protein S13 was deduced from the sequence of **nucleotides** in a recombinant cDNA and confirmed from the NH2-terminal amino acid sequence of the protein. Rat S13 contains 150 amino acids (the NH2-terminal methionine is removed after translation of the mRNA) and has a mol. wt. of 17,080. Hybridization of a S13 cDNA to digests of nuclear DNA suggests that there are 8-10 copies of the gene for the protein. The mRNA for the protein is about 620 **nucleotides** in length. Rat S13 is related to Saccharomyces cerevisiae YS15 and to Halobacterium marismortui **S11**. The protein contains a possible internal duplication of 12 residues.

L13 ANSWER 100 OF 122 SCISEARCH COPYRIGHT 2000 ISI (R)DUPLICATE 25
AN 89:255925 SCISEARCH
GA The Genuine Article (R) Number: U5452
TI COMPLETE **NUCLEOTIDE**-SEQUENCE OF WOUND TUMOR-VIRUS GENOMIC SEGMENT-**S11**

AU DALL D J (reprint); ANZOLA J V; XU Z K; NUSS D L
CS ROCHE INS[illegible]OLEC BIOL, ROCHE RES CTR, NUT[illegible] NJ, 07110 (Reprint)
CYA USA
SO NUCLEIC ACIDS RESEARCH, (1989) Vol. 17, No. 9, pp. 3599.
DT Note; Journal
FS LIFE
LA ENGLISH
REC Reference Count: 5

L13 ANSWER 101 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1990:112956 CAPLUS
DN 112:112956
TI Gene encoding the alpha core subunit of Bacillus subtilis RNA polymerase is cotranscribed with the genes for initiation factor 1 and ribosomal proteins B, S13, **S11**, and L17
AU Boylan, Sharon A.; Suh, Joo Won; Thomas, Susan M.; Price, Chester W.
CS Dep. Food Sci. Technol., Univ. California, Davis, CA, 95616, USA
SO J. Bacteriol. (1989), 171(5), 2553-62.
CODEN: JOBAAY; ISSN: 0021-9193
DT Journal
LA English
AB The genetic and transcriptional organization of the promoter-distal portion of the B. subtilis alpha operon is described. By DNA sequence anal. of the region surrounding rpoA, the gene for the alpha core subunit of RNA polymerase, 6 open reading frames were identified by the similarity of their products to their counterparts in the Escherichia coli transcriptional and translational app. Gene order in this region, given by gene products, was IF1-B-S13-**S11**-alpha-L17. Gene order in E. coli is similar but not identical: SecY-B-S13-**S11**-S4-alpha-L17. The B. subtilis alpha region differed most strikingly from E. coli in the presence of IF1 and the absence of ribosomal proteins S4, which is the translational regulator of the E. coli alpha operon. In place of the gene for S4, B. subtilis had a 177-base-pair intercistronic region contg. 2 possible promoter sequences. However, expts. with S1 mapping of in vivo transcripts, gene disruptions in the alpha region, and a single-copy transcriptional fusion vector all suggested that these possible promoters were largely inactive during logarithmic growth, that the major promoter for the alpha operon lay upstream from the region cloned, and that the genes in the IF1 to L17 interval were contranscribed. Thus, the transcriptional organization of the region resembles that of E. coli, wherein the alpha operon is transcribed primarily from the upstream spc promoter, but the absence of the S4 gene suggests that the translational regulation of the region may differ more fundamentally.

L13 ANSWER 102 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1990:113204 CAPLUS
DN 112:113204
TI Characterization of junD: a new member of the jun proto-oncogene family
AU Hirai, S. I.; Ryseck, R. P.; Mechta, F.; Bravo, R.; Yaniv, M.
CS Dep. Biol. Mol., Inst. Pasteur, Paris, 75724, Fr.
SO EMBO J. (1989), 8(5), 1433-9
CODEN: EMJODG; ISSN: 0261-4189
DT Journal
LA English
AB In an extensive screen of a cDNA library prepd. from serum-stimulated mouse NIH 3T3 cells, 3 distinct jun-related clones were identified. Two clones encoded c-jun and junB sequences resp., whereas the sequence of the third group of clones (junD) was distinct from these 2 and from v-jun. The amino acid sequences derived from these jun-related clones are very well conserved in 5 distinct regions including the putative DNA-binding domain. Truncated c-Jun and JunD proteins contg. the C-terminus recognize

the same DNA sequences which were defined as the PEA1/AP1 binding sequence
or TPA response element (TRE). Furthermore, both can trans-activate a promoter including the TRE, and this activation is further enhanced by c-fos. Contrary to c-jun and junB transcription, which are strongly stimulated by serum or TPA treatment of quiescent 3T3 cells, junD transcription is not significantly stimulated in these conditions. The tissue distribution and levels of expression of junD mRNA differ from that
of c-jun and junB mRNA. These observations suggest that each of these Jun-related gene products has a distinct role in the control of gene activity and growth in the organism.

L13 ANSWER 103 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1989:610788 CAPLUS
DN 111:210788
TI Crosslinking of ribosomal proteins S4, S5, S7, S8, **S11**, S12 and S18 to domains 1 and 2 of 16S rRNA in the Escherichia coli 30S particle
AU Chiaruttini, Claude; Milet, Michele; Hayes, Donal H.; Expert-Bezancon, Alain
CS Lab. Chim. Cell., Inst. Biol. Phys.-Chim., Paris, 75005, Fr.
SO Biochimie (1989), 71(7), 839-52
CODEN: BICMBE; ISSN: 0300-9084
DT Journal
LA English
AB RNA-protein crosslinks were introduced into E. coli 30 S ribosomal subunits by treatment with 1-ethyl-3(3-dimethylaminopropyl)carbodiimide (EDC). Complexes of 16 S rRNA crosslinked to 30 S ribosomal proteins were
isolated and hybridized with a series of single-stranded bacteriophage M13
rDNA probes. These probes, each carrying an inserted rDNA fragment, were used to select contiguous 16 S rRNA sections covering all of domain 1 and the major part of domain 2 (starting at the 5' terminus and ending at **nucleotide** 869) and the proteins covalently linked to each of these sections were identified by 2-dimensional PAGE. This procedure identified proteins S4, S5, S7, S8, **S11**, S12, and S18 as the species most efficiently crosslinked to domains 1 and 2 of 16 S rRNA. These results are discussed in the light of current knowledge of the tertiary structure of 16 S rRNA in the E. coli 30 S ribosomal subunit.

L13 ANSWER 104 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1990:71276 CAPLUS
DN 112:71276
TI The plastid rpoA gene encoding a protein homologous to the bacterial RNA polymerase alpha subunit is expressed in pea chloroplasts
AU Purton, Saul; Gray, John C.
CS Bot. Sch., Univ. Cambridge, Cambridge, CB2 3EA, UK
SO MGG, Mol. Gen. Genet. (1989), 217(1), 77-84
CODEN: MGGEAE; ISSN: 0026-8925
DT Journal
LA English
AB The gene rpoA, encoding a protein homologous to the alpha subunit of RNA polymerase from Escherichia coli has been located in pea chloroplast DNA downstream of the petD gene for subunit IV of the cytochrome b-f complex. **Nucleotide** sequence anal. has revealed that rpoA encodes a polypeptide of 334 amino acid residues with a mol. wt. of 38916. Northern
blot anal. has shown that rpoA is co-transcribed with the gene for ribosomal protein **S11**. A lacZ-rpoA gene-fusion has been constructed and expressed in E. coli. Antibodies raised against the fusion protein have been employed to demonstrate the synthesis of the rpoA
gene product in isolated pea chloroplasts. Western blot anal. using these

antibodies and antibodies against the RNA polymerase core enzyme from the cyanobacterium, Anabaena 7120, has revealed the presence of the gene product in a crude RNA polymerase prepn. from pea chloroplasts.

L13 ANSWER 105 OF 122 SCISEARCH COPYRIGHT 2000 ISI (R)DUPLICATE 26
AN 88:607783 SCISEARCH
GA The Genuine Article (R) Number: Q7448
TI MOLECULAR-CLONING AND **NUCLEOTIDE**-SEQUENCE OF THE GENE FOR THE RIBOSOMAL PROTEIN-**S11** FROM THE ARCHAEBACTERIUM HALOBACTERIUM-MARISMORTUI
AU ARNDT E (Reprint); KIMURA M
CS MAX PLANCK INST MOLEC GENET, WITTMANN ABT, D-1000 BERLIN 33, FED REP GER (Reprint)
CYA GERMANY
SO JOURNAL OF BIOLOGICAL CHEMISTRY, (1988) Vol. 263, No. 31, pp. 16063-16068.
DT Article; Journal
FS LIFE
LA ENGLISH
REC Reference Count: 19

L13 ANSWER 106 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1988:487217 CAPLUS
DN 109:87217
TI Sequence of a cloned cDNA encoding human ribosomal protein **S11**
AU Lott, John B.; Mackie, George A.
CS Dep. Biochem., Univ. West. Ontario, London, ON, N6A 5C1, Can.
SO Nucleic Acids Res. (1988), 16(3), 1205
CODEN: NARHAD; ISSN: 0305-1048
DT Journal
LA English
AB A cloned cDNA that encodes human ribosomal protein **S11** was isolated and sequenced. The predicted amino acid sequence of 158 residues is identical to that of rat **S11**. The **nucleotide** sequence in the coding region differs, however, from that of the rat in the 1st position in 2 codons and in the 3rd position in 44 codons.

L13 ANSWER 107 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1988:469156 CAPLUS
DN 109:69156
TI Interaction of ribosomal proteins S5, S6, **S11**, S12, S18 and S21 with 16 S rRNA
AU Stern, Seth; Powers, Ted; Changchien, Li-Ming; Noller, Harry F.
CS Thimann Lab., Univ. California, Santa Cruz, CA, 95064, USA
SO J. Mol. Biol. (1988), 201(4), 683-95
CODEN: JMOBAK; ISSN: 0022-2836
DT Journal
LA English
AB The effects of assembly of ribosomal proteins S5, S6, **S11**, S12, S18, and S21 on the reactivities of residues in 16 S rRNA toward chem. probes were examd. S6, S18, and **S11** interact with the 690-720 and 790 loop regions of 16 S rRNA in a highly cooperative manner, that is consistent with the previously defined assembly map relationships among these proteins. The results also indicate that these proteins, one of which (S18) has previously been implicated as a component of the ribosomal P-site, interact with residues near some of the recently defined P-site (class II tRNA protection) **nucleotides** in 16 S rRNA. In addn., assembly of protein S12 resulted in the protection of residues in both the 530 stem/loop and the 900 stem regions; the latter group is closely juxtaposed to a segment of 16 S rRNA recently shown to be protected from chem. probes by streptomycin. Interestingly, both S5 and S12 appear to protect, to differing degrees, a well-defined set of residues in the 900

stem/loop and 5'-terminal regions. These observations are discussed in terms of the effects of S5 and S12 on streptomycin binding, and in terms of the class III tRNA protection found in the 900 stem of 16 S rRNA. Altogether these results show that many of the small subunit proteins, which have previously been shown to be functionally important, appear to be assocd. with functionally implicated segments of 16 S rRNA.

L13 ANSWER 108 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1989:451419 CAPLUS
DN 111:51419
TI **Nucleotide** sequence of maize chloroplast RPS11 with conserved amino acid sequence between eukaryotes, bacteria and plastids
AU Markmann-Mulisch, Ulrich; Subramanian, Alap Raman
CS Abt. Wittmann, Max-Planck-Inst. Mol. Genet., Berlin, D-1000/33, Fed. Rep. Ger.
SO Biochem. Int. (1988), 17(4), 655-64
CODEN: BIINDF; ISSN: 0158-5231
DT Journal
LA English
AB **Nucleotide** sequence of a 721-base-pair segment of maize chloroplast DNA, encoding the putative chloroplast ribosomal protein **S11** at phys. map position 33.1-33.5 Kbp, is described. A Shine-Dalgarno sequence and computer-derived stem-loop structures of dyad symmetry are present in the spacer region between rpS11 and its 5' upstream gene rpL36. The deduced amino acid sequence of maize chloroplast **S11** shows 69%, 66%, 62%, 57%, 48%, and 45% sequence identity to the corresponding sequences of tobacco, spinach, pea, liverwort, Escherichia coli, and Bacillus subtilis, resp., and 41% sequence identity to 3 eukaryotic cytoplasmic ribosomal proteins, S14 of Chinese hamster and of human, and rp59 of yeast. Maize chloroplast ribosomal protein **S11** is larger than the other published S11s of plants and bacteria, due to the apparent tandem introduction of a short sequence stretch of internal homol.

L13 ANSWER 109 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1989:109255 CAPLUS
DN 110:109255
TI Structure and organization of Marchantia polymorpha chloroplast genome. III. Gene organization of the large single copy region from rbcL to trnI(CAU)
AU Fukuzawa, Hideya; Kohchi, Takayuki; Sano, Toru; Shirai, Hiromasa; Umesono, Kazuhiko; Inokuchi, Hachiro; Ozeki, Haruo; Ohyama, Kanji
CS Fac. Agric., Kyoto Univ., Kyoto, 606, Japan
SO J. Mol. Biol. (1988), 203(2), 333-51
CODEN: JMOBAK; ISSN: 0022-2836
DT Journal
LA English
AB The **nucleotide** sequence (25,320 base-pairs) of a part of the large single-copy region of chloroplast DNA from the liverwort M. polymorpha was detd. This region encodes putative genes for four tRNAs, isoleucine tRNACAU, arginine tRNACCG, proline tRNAUGG, and tryptophan tRNACCA; eight photosynthetic polypeptides, the large subunit of ribulose bisphosphate carboxylase/oxygenase (rbcL), 51,000 Mr photosystem II chlorophyll a apoprotein (psbB), apocytochrome b-559 polypeptides (psbE and psbF), 10,000 Mr phosphoprotein (psbH), cytochrome f preprotein (petA), cytochrome b6 polypeptide (petB), and cytochrome b6/f complex subunit 4 polypeptide (petD); 13 ribosomal proteins (L2, L14, L16, L20, L22, L23, L33, S3, S8, **S11**, S12, S18, and S19); initiation factor 1 (infA); ribosome-assocg. polypeptide (secX); and .alpha. subunit of RNA polymerase (rpoA). Functionally related genes were located in several clusters in this region of the genome. There were two ribosomal protein gene clusters: rpl23-rpl2-rps19-rpl22-rps3-rpl16-rpl14-rps8-infA-

secX-rps11-[redacted]poA, with a gene arrangement similar to that of the Escherichi[redacted]oli S10-spc-.alpha. operons, a[redacted]the rps12'-rpl20-rps18-rpl33 cluster. There were gene clusters encoding photosynthesis components such as the psbB-psbH-petB-petD, and the psbE-psbF clusters. Thirteen open reading frames, ranging in length from 31 to 434 amino acid residues, remain to be identified.

L13 ANSWER 110 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1988:144410 CAPLUS
DN 108:144410
TI **Nucleotide** sequence of the gene for ribosomal protein L36 in pea chlorplast DNA
AU Purton, Saul; Gray, John C.
CS Bot. Sch., Univ. Cambridge, Cambridge, CB2 3EA, UK
SO Nucleic Acids Res. (1987), 15(21), 9080
CODEN: NARHAD; ISSN: 0305-1048
DT Journal
LA English
AB **Nucleotide** sequence anal. upstream of the gene (rps11) for the ribosomal protein **S11** in pea chloroplast DNA has revealed a small open reading frame (ORF) of 37 codons. The ORF encodes a very basic protein of mol. wt. 4328 which shows 73% homol. to a ribosomal protein from Bacillus stearothermophilus and 62% homol. to the deduced amino acid sequence of the Escherichia coli gene, X, located at the end of the spc operon. X has recently been identified as a component of the ribosomal 50 S subunit. The ORF has been sequenced also in the chloroplast genomes of spinach, tobacco and liverwort where it is referred to as secX. In accordance with the suggested nomenclature for chloroplast genes, the authors proposed to call it rpl36.

L13 ANSWER 111 OF 122 SCISEARCH COPYRIGHT 2000 ISI (R)DUPLICATE 27
AN 87:118085 SCISEARCH
GA The Genuine Article (R) Number: G2082
TI **NUCLEOTIDE**-SEQUENCE OF THE GENE FOR RIBOSOMAL-PROTEIN **S11** IN PEA CHLOROPLAST DNA
AU PURTON S (Reprint); GRAY J C
CS UNIV CAMBRIDGE, SCH BOT, DOWNING ST, CAMBRIDGE CB2 3EA, ENGLAND (Reprint)
CYA ENGLAND
SO NUCLEIC ACIDS RESEARCH, (1987) Vol. 15, No. 4, pp. 1873.
DT Note; Journal
FS LIFE
LA ENGLISH
REC Reference Count: 5

L13 ANSWER 112 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1987:510230 CAPLUS
DN 107:110230
TI Structure and expression of the Saccharomyces cerevisiae CRY1 gene: a highly conserved ribosomal protein gene
AU Larkin, John C.; Thompson, J. Ryan; Woolford, John L., Jr.
CS Dep. Biol. Sci., Carnegie Mellon Univ., Pittsburgh, PA, 15213, USA
SO Mol. Cell. Biol. (1987), 7(5), 1764-75
CODEN: MCEBD4; ISSN: 0270-7306
DT Journal
LA English
AB The S. cerevisiae (CRY1 gene encodes ribosomal protein rp59, a component of the 40S ribosomal subunit. Mutations in CRY1 can confer resistance to the alkaloid cryptopleurine, an inhibitor of the elongation step of translation. The **nucleotide** sequence of the cloned CRY1 gene was detd. The predicted amino acid sequence shows that CRY1 encodes a 14,561-dalton polypeptide that has 88% amino acid sequence homol. to the

hamster or human S14 ribosomal protein responsible for emetine resistance and 45% ho[illegible]. to Escherichia coli ribosomal protein **S11**. Anal. of the DNA sequences upstream from CRY1 revealed the presence of three sequences, HOMOL1 (consensus, A/TACATCC/TG/ATA/GCA), RPG (consensus, ACCCA/GTACATT/CT/A), and a thymine-rich sequence, found upstream of more than 20 other cloned yeast genes encoding components of the translational app. The ability to assay the expression of CRY1 in vivo by using the cryptopleurine resistance phenotype was exploited to demonstrate that these three consensus sequences are necessary for the transcription of CRY1. The upstream promoter element of the yeast RP39A gene consists of these identical sequence motifs. Therefore, these three sequences may define a consensus promoter element for the genes encoding the yeast translational app. CRY1 Is one of several hundred yeast genes, including ribosomal protein genes, whose expression is transiently decreased 10-fold upon heat shock. The HOMOL1 and RPG consensus sequences are not necessary for the heat shock response of CRY1.

L13 ANSWER 113 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1987:613657 CAPLUS
DN 107:213657
TI S4-.alpha. mRNA translation repression complex. I. Thermodynamics of formation
AU Deckman, Ingrid C.; Draper, David E.; Thomas, Mark S.
CS Dep. Chem., Johns Hopkins Univ., Baltimore, MD, 21218, USA
SO J. Mol. Biol. (1987), 196(2), 313-22
CODEN: JMOBAK; ISSN: 0022-2836
DT Journal
LA English
AB The expression of the 4 ribosomal proteins from the Escherichia coli .alpha. operon (S4, **S11**, S13, and L17) is regulated at the level of translation by the binding of S4 to the .alpha. mRNA. Using a filter binding assay and .alpha. mRNA sequences prepd. by in vitro transcription, previous work located the S4 target site within the .apprx.100-base leader sequence. This work was extended to include fragments of the .alpha. leader with 6 different 5' end points and 4 different 3' end points. A core region between bases 23 and 69 (numbering from the 1st **nucleotide** of the E. coli transcript) bound S4 with an affinity of .apprx.2 .mu.M-1. Regions of weak interactions were located in the 22 **nucleotides** 5' and 70 **nucleotides** 3' to this core; they increased the S4 affinity to .apprx.13 .mu.M-1. Studies of S4-.alpha. mRNA binding under different conditions revealed the following. (1) Specific and nonspecific binding showed the same dependence on K+ concn. in most K salts. With KCl and KBr, much weaker salt dependence of specific complex formation was obsd. suggesting that the protein responds to the correct RNA substrate by binding halide anions. (2) Increasing the MgCl2 concn. between 1 and 4 mM enhanced the binding by 4-fold with no further effects up to 20 mM. About 5 Mg2+ were taken up by the complex with an av. binding const. of .apprx.600 M-1 each. Renaturation of the RNA in the presence of MgCl2 was also required to obtain full binding. These effects were seen only with .alpha. mRNA extending beyond the initiation codon; S4 binding to the .alpha. leader sequence itself was insensitive to Mg2+. (3) The assocn. kinetics were fast and probably diffusion-controlled. (4) The formation of the complex was entirely entropy-driven.

L13 ANSWER 114 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1987:97363 CAPLUS
DN 106:97363
TI The genes for ribosomal protein S14. I. Sequence of wild-type and emtB mutants in Chinese hamster ovary cells. II. Sequence of the

transcriptionally active gene on human chromosome 5. III. Evolutionary homologs in yeast and bacteria

AU Rhoads, Douglas Duane
CS Kansas State Univ., Manhattan, KS, USA
SO (1986) 103 pp. Avail.: Univ. Microfilms Int., Order No. DA8624666
From: Diss. Abstr. Int. B 1987, 47(7), 2754
DT Dissertation
LA English
AB Unavailable

L13 ANSWER 115 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1986:162786 CAPLUS
DN 104:162786
TI Spinach plastid genes coding for initiation factor IF-1, ribosomal protein **S11** and RNA polymerase .alpha.-subunit

AU Sijben-Mueller, Gertrud; Hallick, Richard B.; Alt, Juliane; Westhoff, Peter; Herrmann, Reinhold G.
CS Bot. Inst., Univ. Duesseldorf, Duesseldorf, 4000, Fed. Rep. Ger.
SO Nucleic Acids Res. (1986), 14(2), 1029-44
CODEN: NARHAD; ISSN: 0305-1048
DT Journal
LA English
AB The **nucleotide** sequence of 2.5 kilobase pair (kbp) from the cloned SalI fragments 8 and 11 of spinach plastid DNA was detd. This region was found to encode 3 open reading frames for hydrophilic polypeptides of 77, 138, and 335 amino acids. Using the computer search algorithm of D. J. Lipman and W. R. Pearson (1985), these genes were identified as coding for homologs of Escherichia coli initiation factor IF-1 (infA), 30 S ribosomal protein **S11** (rps11), and the .alpha.-subunit of DNA-dependent RNA polymerase (rpoA) [9014-24-8]. The spinach plastid gene organization is infA - 381 bp spacer - rps11 - 72 bp spacer - rpoA. The genes are transcribed in vivo and appear to encode functional proteins. These findings imply that plastid chromosomes code for components of the organelle transcription app.

L13 ANSWER 116 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1987:13750 CAPLUS
DN 106:13750
TI Gene for the alpha subunit of Bacillus subtilis RNA polymerase maps in the ribosomal protein gene cluster

AU Suh, Joo Won; Boylan, Sharon A.; Price, Chester W.
CS Dep. Food Sci. Technol., Univ. California, Davis, CA, 95616, USA
SO J. Bacteriol. (1986), 168(1), 65-71
CODEN: JOBAAY; ISSN: 0021-9193
DT Journal
LA English
AB The gene encoding the alpha subunit of B. subtilis RNA polymerase [9014-24-8] was isolated from a .lambda.gt11 expression vector library by using anti-alpha antibody as a probe. Four unique clones were isolated, one carrying a lacZ-alpha gene fusion and the others carrying the entire alpha coding region together with addnl. sequences upstream. The identity of the cloned alpha gene was confirmed by the size and immunol. reactivity of its product expressed in Escherichia coli. Further, a partial DNA sequence found the predicted N terminus of alpha homologous with E. coli alpha. By plasmid integration and PBS1 transduction, alpha was near rspE and within the major ribosomal protein gene cluster on the B. subtilis chromosomes. Addnl. DNA sequencing identified rpsM (encoding S13) and rpsK (encoding **S11**) upstream of alpha, followed by a 180-base-pair intercistronic region that may contain 2 alpha promoters. Although the organization of the alpha region resembles that of the alpha operon of E. coli, the putative promoters and absence of rpsD (encoding

S4) immediately preceding the B. subtilis alpha gene suggest a different regulation

L13 ANSWER 117 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1987:62128 CAPLUS
DN 106:62128
TI The genes encoding chloroplast ribosomal proteins S7 and S12 are located in the inverted repeat of Spirodela oligorhiza chloroplast DNA
AU Posno, Mark; Verweij, Wim R.; Dekker, Ilma C.; De Waard, Philip M.; Groot, Gert S. P.
CS Biochem. Lab., Free Univ. Amsterdam, Amsterdam, NL-1081 HV, Neth.
SO Curr. Genet. (1986), 11(1), 25-34
CODEN: CUGED5; ISSN: 0172-8083
DT Journal
LA English
AB A variety of methods was used to localize the genes for ribosomal proteins S7 and S12 on Spirodela chloroplast DNA. Heterologous hybridization with a rps12 gene specific probe from Euglena has revealed the presence of rps12 homologous sequences within the inverted repeat of Spirodela chloroplast DNA on the fragment BamHI-V. In the partial **nucleotide** sequence of this fragment, 2 regions of amino acid sequence homol. to Euglena S12 can be identified, sepd. from each other by a 542 base-pair (bp) intron with conserved boundary sequences. As was found for Nicotiana S12, the Spirodela S12 coding regions are for 85 amino acids homologous (79%) to Escherichia coli S12 (starting from residue 38 to the C-terminus). Likewise, the 37 5' terminal codons of rps12 in Spirodela were not identified. The functionality of the Spirodela rps12 sequence is discussed. The rps7 gene is located adjacent to rps12. Chloroplast ribosomal protein C-**S11** (homologous to S7) was detected by immunopptn. with both a polyspecific anti-30 S serum and an anti C-**S11** serum, among the in vitro translation products of mRNAs selected by Spirodela chloroplast DNA fragments BamHI-V and BamHI-P.
Since in a DNA dependent E. coli cell-free system, only BamHI-V appears to be capable of synthesis of C-**S11**, it is concluded that rps7 is located entirely within BamHI-V and is transcribed into a mRNA which extends into BamHI-P. As detd. by Northern hybridization expts., rps7 is cotranscribed with rps12; a stable transcript of .apprx.1100 **nucleotide** bases (b) is detected in total cellular Spirodela RNA with either rps12 and rps7 gene-specific probes. The rps12 probe addnl. detects an .apprx.600 b transcript, which presumably corresponds to the excised rps12 intron RNA. Finally the expression of both rps7 and rps12 was examd. during light-induced chloroplast development by Northern blotting and by immunoblotting. The steady-state levels of neither chloroplast ribosomal protein transcripts, nor those of the chloroplast ribosomal proteins itself, changed significantly during the greening process.

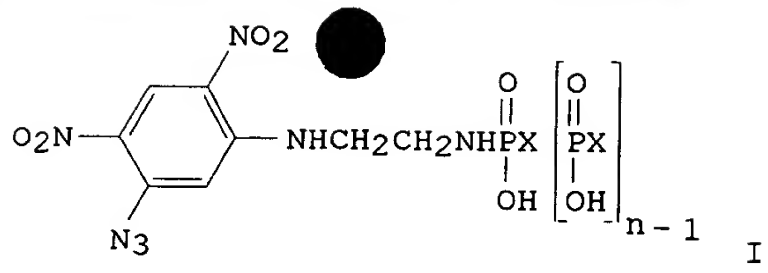
L13 ANSWER 118 OF 122 SCISEARCH COPYRIGHT 2000 ISI (R) DUPLICATE 28
AN 85:278630 SCISEARCH
GA The Genuine Article (R) Number: AHT22
TI **NUCLEOTIDE**-SEQUENCE OF CLONED CDNA SPECIFIC FOR RAT RIBOSOMAL PROTEIN-**S11**
AU TANAKA T (Reprint); KUWANO Y; ISHIKAWA K; OGATA K
CS YAMAGATA UNIV, SCH MED, DEPT BIOCHEM, YAMAGATA 99023, JAPAN (Reprint); NIIGATA UNIV, SCH MED, DEPT BIOCHEM, NIIGATA 951, JAPAN
CYA JAPAN
SO JOURNAL OF BIOLOGICAL CHEMISTRY, (1985) Vol. 260, No. 10, pp. 6329-6333.
DT Article; Journal
FS LIFE

LA ENGLISH
REC Reference count: 39

L13 ANSWER 119 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1985:482528 CAPLUS
DN 103:82528
TI **Nucleotide** sequence of the alpha ribosomal protein operon of Escherichia coli
AU Bedwell, David; Davis, Geneva; Gosink, Mark; Post, Leonard; Nomura, Masayasu; Kestler, Harry; Zengel, Janice M.; Lindahl, Lasse
CS Inst. Enzyme Res., Univ. Wisconsin, Madison, WI, 53706, USA
SO Nucleic Acids Res. (1985), 13(11), 3891-903
CODEN: NARHAD; ISSN: 0305-1048
DT Journal
LA English
AB In E. coli some 19 transcription units encoding the 52 ribosomal proteins are scattered throughout the genome. One of the units, the .alpha. operon, encodes genes for the ribosomal proteins S13, **S11**, S4, and L17 as well as the kilobase subunit of RNA polymerase [9014-24-8]. The complete 3.0-kilobase **nucleotide** sequence of the .alpha. operon is reported. In addn., the site of transcription termination in this operon was detd.

L13 ANSWER 120 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1984:605016 CAPLUS
DN 101:205016
TI **Nucleotide** sequence of the rpoA-rplQ DNA of Escherichia coli: a second regulatory binding site for protein S4?
AU Meek, David W.; Hayward, Richard S.
CS Dep. Mol. Biol., Univ. Edinburgh, Edinburgh, EH9 3JR, UK
SO Nucleic Acids Res. (1984), 12(14), 5813-21
CODEN: NARHAD; ISSN: 0305-1048
DT Journal
LA English
AB The .alpha.-operon of Escherichia coli is a unit of regulation comprising the following known genes, mostly encoding ribosomal proteins (in the order of transcription, and with their products named in brackets): rpsM (S13), rpsK (**S11**), rpsD (S4), rpoA (.alpha.-subunit of RNA polymerase [9014-24-8]), and rplQ (L17). There is evidence that S4 tightly regulates all of these genes, except rpoA, by repressing translation of the polycistronic mRNA. Binding of S4 to the S13 start site is thought to regulate the 1st 3 genes. The rpsD-rpoA sequences previously detd. by other were extended to include all of rpoA and rplQ. The rpoA-rplQ intercistronic region shows strong primary and potential secondary structural homologies with the S4-binding sites on 16 S rRNA and S13 mRNA. Perhaps S4 represses L17 translation directly.

L13 ANSWER 121 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1984:586326 CAPLUS
DN 101:186326
TI Affinity labeling of ribosomes from Escherichia coli with photoactivated analogs of mRNA
AU Gimautdinova, O. I.; Zenkova, M. A.; Karpova, G. G.; Podust, L. M.
CS Inst. Org. Chem., Novosibirsk, USSR
SO Mol. Biol. (Moscow) (1984), 18(4), 907-18
CODEN: MOBIBO; ISSN: 0026-8984
DT Journal
LA Russian
GI



I

AB Oligonucleotide [2-(N-2,4-dinitro-5-azidophenyl)aminoethyl]phosphamides (I, where X = nucleoside and n = total no. of X units) were prepd. and used as mRNA analogs to photoaffinity label E. coli ribosomes. Up to 10% of I, bound in the tRNA-ribosome-I complex, is crosslinked with ribosomal proteins of the 30 S and 50 S subunits. I (where X = uridine and n = 4, 7, or 8), which did not modify rRNA, modified proteins S3, S4, S9, **S11**, S12, S14, S17, S19, and S20 in the 30 S subunit and proteins L2, L13, L16, L27, L32, and L33 in the 50 S subunit. The specific proteins modified depended on oligonucleotide length, and the modification required the presence of tRNA in the ribosome A site.

L13 ANSWER 122 OF 122 CAPLUS COPYRIGHT 2000 ACS
AN 1980:490412 CAPLUS
DN 93:90412
TI DNA sequence of the promoter region for the .alpha. ribosomal protein operon in Escherichia coli
AU Post, Leonard E.; Arfsten, Ann E.; Davis, Geneva R.; Nomura, Masayasu
CS Inst. Enzyme Res., Univ. Wisconsin, Madison, WI, 53706, USA
SO J. Biol. Chem. (1980), 255(10), 4653-9.
CODEN: JBCHA3; ISSN: 0021-9258
DT Journal
LA English
AB Previous studies showed that the gene for RNA polymerase subunit .alpha. at 72 min on the E. coli chromosome is co-transcribed with genes for ribosomal proteins (r-proteins) **S11**, S4, and L17, and probably S13. DNA sequence anal. of a deletion mutant established that the S13 gene is a part of the .alpha. operon and the gene order is promoter (P.alpha.), rpsM (S13), rpsK (**S11**), rpsD (S4), rpoA (.alpha.), and rplQ (L17). The DNA sequence extending 650 bases before S13 gene was detd. In vitro transcription expts. establish the probable location of the .alpha. promoter (P.alpha.) within this sequence. The start site is 94 **nucleotides** upstream from the initiation codon (GUG) of the S13 gene. This promoter had features previously noted as common to E. coli promoters. However, comparison with 4 other sequenced promoters of r-protein operons shows no unique common features that might account for the common regulation of synthesis of r-proteins. This lack of sequence similarity in promoters of r-protein operons may be because r-protein synthesis is regulated at least partially at a post-transcriptional level.

=> display l14 1-11 bib abs

L14 ANSWER 1 OF 11 CAPLUS COPYRIGHT 2000 ACS
AN 1998:559055 CAPLUS
DN 129:171765
TI Method of genome dactyloscopy
IN Sverdlov, Evgenij D.; Potapov, Viktor K.; Veselovskaya, Svetlana V.; Myasnikov, Viktor A.; Limborskaya, Svetlana A.; Prosnyak, Mikhail I.; Efremova, Evgeniya Yu.
PA Institut Molekulyarnoj Genetiki RAN, Russia
SO Russ.
From: Izobreteniya 1997, (29), 310.

CODEN: RUX[illegible]7
DT Patent
LA Russian
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI RU 2093582	C1	19971020	RU 1993-37516	19930721

AB The invention concerns a method to use genomes for dactyloscopy by fragmenting DNA and hybridizing with labeled oligo or polynucleotides and comparing the result with a control sample. The nucleotide contains 5-methyldeoxycytidine and **2-aminodeoxyadenosine**, preferably an oligonucleotide contg. these.

L14 ANSWER 2 OF 11 SCISEARCH COPYRIGHT 2000 ISI (R) DUPLICATE 1
AN 95:154003 SCISEARCH
GA The Genuine Article (R) Number: QH930
TI HYDROPHOBIC, NON-HYDROGEN-BONDING BASES AND BASE-PAIRS IN DNA
AU SCHWEITZER B A; KOOL E T (Reprint)
CS UNIV ROCHESTER, DEPT CHEM, ROCHESTER, NY, 14627 (Reprint); UNIV ROCHESTER,
DEPT CHEM, ROCHESTER, NY, 14627
CYA USA
SO JOURNAL OF THE AMERICAN CHEMICAL SOCIETY, (22 FEB 1995) Vol. 117, No. 7, pp. 1863-1872.
ISSN: 0002-7863.
DT Article; Journal
FS PHYS; LIFE
LA ENGLISH
REC Reference Count: 56
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS
AB We report the properties of hydrophobic isosteres of pyrimidines and purines in synthetic DNA duplexes. Phenyl nucleosides 1 and 2 are nonpolar isosteres of the natural thymidine nucleoside, and indole nucleoside 3 is an analog of the complementary purine **2-aminodeoxyadenosine**. The nucleosides were incorporated into synthetic oligodeoxynucleotides and were paired against each other and against the natural bases. Thermal denaturation experiments were used to measure the stabilities of the duplexes at neutral pH. It is found that the hydrophobic base analogs ate nonselective in pairing with the four natural bases but selective for pairing with each other rather than with the natural bases, For example, compound 2 selectively pairs with itself rather than with A, T, G, or C; the magnitude of this selectivity is found to be 6.5-9.3 degrees C in T-m or 1.5-1.8 kcal/mol in free energy (25 degrees C). All possible hydrophobic pairing combinations of 1, 2, and 3 were examined, Results show that the pairing affinity depends on the nature of the pairs and on position in the duplex. The highest affinity pairs are found to be the 1-1 and 2-2 self-pairs and the 1-2 heteropair. The best stabilization occurs when the pairs are placed at the ends of duplexes rather than internally; the internal pairs may be destabilized by imperfect steric mimicry which leads to non-ideal duplex structure. In some cases the hydrophobic pairs are significantly stabilizing to the DNA duplex; for example, when situated at the end of a duplex, the 1-1 pair is more stabilizing than a T-A pair. When situated internally, the affinity of the 1-1 pair is the same as, or slightly better than, the analogous T-T mismatch pair, which is known to have two hydrogen bonds. The studies raise the possibility that hydrogen bonds may not always be required for the formation of stable duplex DNA-like structure, In addition, the results point out the importance of solvation and desolvation in natural base pairing, and lend new support to the idea that hydrogen bonds in DNA may be mon important for specificity of pairing than for affinity,

Finally, the study raises the possibility of using these or related base pairs to expand the genetic code beyond the natural A-T and G-C pairs.

L14 ANSWER 3 OF 11 CAPLUS COPYRIGHT 2000 ACS
AN 1995:605276 CAPLUS
DN 123:47455
TI Antiviral activity of 2-aminoadenosine, **2-aminodeoxyadenosine** and their N6-substituted derivatives in Vero cells
AU Fujita, Haruhisa; Muraoka, Masako
CS Sch. Med., Keio Univ., Tokyo, 160, Japan
SO Oyo Yakuri (1995), 49(6), 627-34
CODEN: OYYAA2; ISSN: 0300-8533
DT Journal
LA Japanese
AB 2-Aminoadenosine (n2A), **2-aminodeoxyadenosine** (dn2A) and their N6-substituted derivs. were examd. for their antiviral activity in Vero cells. As for RNA viruses, Coxsackie virus type B-5 and Echo virus type 9 were used; as for DNA viruses, herpes simplex viruses (HSV) type 1 and HSV type 2 were used. Among the compds. tested, dn2A had dose-dependent antiviral activity against herpes simples virus type 2 and weak antiviral activity against herpes simplex virus type 1. Moreover, N6-cyclohexyl-n2A and N6-cyclohexyl-dn2A weakly inhibited the cytopathic effect of HSV type 1 and HSV type 2. On the other hand, n2A had weak antiviral activity against Coxsakie virus B-5 and 3',5'-O-TDPS-8-OH-n2A weakly inhibited the cytopathic effect of Coxsakie virus type B-5 and Echo virus type 9.

L14 ANSWER 4 OF 11 SCISEARCH COPYRIGHT 2000 ISI (R) DUPLICATE 2
AN 95:4830 SCISEARCH
GA The Genuine Article (R) Number: PV566
TI AROMATIC NONPOLAR NUCLEOSIDES AS HYDROPHOBIC ISOSTERES OF PYRIMIDINE AND PURINE NUCLEOSIDES
AU SCHWEITZER B A; KOOL E T (Reprint)
CS UNIV ROCHESTER, DEPT CHEM, ROCHESTER, NY, 14627 (Reprint); UNIV ROCHESTER, DEPT CHEM, ROCHESTER, NY, 14627
CYA USA
SO JOURNAL OF ORGANIC CHEMISTRY, (02 DEC 1994) Vol. 59, No. 24, pp. 7238-7242.
ISSN: 0022-3263.
DT Article; Journal
FS PHYS; LIFE
LA ENGLISH
REC Reference Count: 28
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS
AB Described are the design, synthesis, and structures of three nonpolar nucleoside isosteres to be used as probes of noncovalent bonding in DNA and as isosteric replacements for the natural nucleosides in designed nucleic acid structures. Reaction of substituted aryl Grignards with 3',5'bis-O-toluoyl-alpha-deoxyibofufanosyl chloride and subsequent deprotection with sodium methoxide in methanol afforded the two beta-C-nucleoside pyrimidine analogs 1 and 2. The dimethylindolyl nucleoside 3, a purine isostere, was obtained by a nucleophilic displacement on alpha-chlorodeoxyribofuranose by the sodium salt of 4,6-dimethylindole, followed by deprotection. Regio- and stereochemistry of the products were established with NOE difference spectra and H-1 NMR splitting patterns. Analogs 1 and 2 are nonpolar isosteres of thymidine, and nucleoside 3 is an isostere of **2-aminodeoxyadenosine**, the triply-bonded Watson-Crick partner of thymidine. Semiempirical AM1 calculations were carried out to provide bond length information to assess structural similarities between the isosteres and their natural counterparts.

L14 ANSWER 5 OF 11 CAPLUS COPYRIGHT 2000 ACS
AN 1995:76381 CAPLUS
DN 122:2082
TI Comparison of genomes by polymerase chain reaction with random priming by oligonucleotide analogs forming tightly-binding duplexes
AU Lebedev, Yu. B.; Shevchenko, Yu.; Potapov, V. K.; Myasnikov, V. A.; Veselovskaya, S. V.; Brikun, I.; Berg, D.; Sverdlov, E. D.
CS Inst. Bioorg. Khim. im. M. M. Shemyakina, Moscow, Russia
SO Dokl. Akad. Nauk (1994), 335(6), 799-801
CODEN: DAKNEQ
DT Journal
LA Russian
AB 5-Methyldeoxycytidine (m5dC) and **2-aminodeoxyadenosine** (am2dA) were used in the construction of random primers for polymerase chain reaction anal. of genomic DNA. Polymerase chain reaction cycles using the modified primers could be run at higher temps. and shorter times than those using unmodified primers.

L14 ANSWER 6 OF 11 CAPLUS COPYRIGHT 2000 ACS
AN 1994:70346 CAPLUS
DN 120:70346
TI Oligonucleotides forming highly stable specific duplexes: their use as primers in sequencing and in the polymerase chain reaction
AU Azhikina, T. L.; Shevchenko, Yu. O.; Lebedev, Yu. B.; Veselovskaya, S. V.; Myasnikov, V. A.; Potapov, V. K.; Sverdlov, E. D.
CS Inst. Bioorg. Khim. im. Shemyakina, Moscow, Russia
SO Dokl. Akad. Nauk (1993), 330(5), 642-5 [Biochem.]
CODEN: DAKNEQ
DT Journal
LA Russian
AB Oligonucleotides contg. 5-methyldeoxycytosine (m5C) and **2-aminodeoxyadenosine** (am2A) were used as primers in DNA sequencing and RAPD (random amplified polymorphic DNA) polymerase chain reaction. Using the modified primers enhanced priming efficiency in sequencing. The classical model of initiation of DNA formation by DNA polymerase Pol I or Taq types was discussed with regard to the initiating complex stability. The utility of the modified primers in RAPD was demonstrated.

L14 ANSWER 7 OF 11 CAPLUS COPYRIGHT 2000 ACS
AN 1987:33420 CAPLUS
DN 106:33420
TI Synthesis and properties of phosphoramidite derivatives of modified nucleosides
AU Tanaka, Toshiki; Tamatsukuri, Sigeru; Ikehara, Morio
CS Fac. Pharm. Sci., Osaka Univ., Osaka, 565, Japan
SO Chem. Pharm. Bull. (1986), 34(5), 2044-8
CODEN: CPBTAL; ISSN: 0009-2363
DT Journal
LA English
OS CASREACT 106:33420
AB Protected N6-methyl-2'-deoxyadenosine (d-m6A), 2-amino-2'-deoxyadenosine (d-a2A), 2'-deoxyinosine (dI), 5-methyl-2'-deoxycytidine (d-m5C) and deoxyuridine (dU) were reacted with bis(diisopropylamino)methoxyphosphine in the presence of diisopropylammonium tetrazolide as the activating reagent to give the corresponding phosphoramidite derivs. in yields of 100, 65, 70, 78 and 65%, resp. The 31 P-NMR spectra of the products were measured. Using these compds., dinucleotides and trinucleotides were synthesized on a long-chain alkylamine controlled pore glass in quant. yields. The stability of 6-methyldeoxyadenosine and N,N-diisobutyryl-**2-aminodeoxyadenosine** to acid was exam'd. When protected di- and trinucleotides (m6A-T, a2A-T, T-m6A-T, T-a2A-T) bound to the

support were treated with 3% trichloroacetic acid in CH2Cl2 depurination was negligible within 10 min (dinucleotide) or 60 min (trinucleotide).

L14 ANSWER 8 OF 11 CAPLUS COPYRIGHT 2000 ACS
AN 1986:144141 CAPLUS
DN 104:144141
TI Influence of 2-aminoadenosine, A', on the conformational behavior of d(T-A'-T-A'). A one-dimensional proton NMR study at 300 MHz and 500 MHz
AU Rinkel, Lambertus J.; Mellema, Jan Remt; Van der Marel, Gijs A.; Van Boom, Jacques H.; Altona, Cornelis
CS Gorlaeus Lab., State Univ. Leiden, Leiden, NL-2300 RA, Neth.
SO Eur. J. Biochem. (1986), 154(2), 259-65
CODEN: EJBCAI; ISSN: 0014-2956
DT Journal
LA English
AB 1H-NMR studies at 300 and 500 MHz in aq. soln. were carried out on the modified self-complementary tetranucleoside triphosphate d(T-A'-T-A'), where d(A') is **2-aminodeoxyadenosine**. NMR spectra were obsd. at 2 sample concns. over the temp. range 2-70.degree.. Assignments based on homonuclear decoupling and nuclear Overhauser enhancement (NOE) expts. are given. The concn. dependence of the chem. shift vs. temp. profiles was used to ext. information concerning duplex formation. The 1H-1H and 1H-P coupling consts. were obtained at 4 temps. and yielded accurate conformational data on the sugar ring and on the back-bone angles .beta., .gamma., and .delta.. The obsd. line broadening, shift profiles, NOEs, and the presence of imino 1H resonances, suggest that the compd. exists as a mini-duplex at low temp. Comparison of these observations with similar observations on the parent compd. d(T-A-T-A) indicate that substitution of dA by dA' increases the tendency towards duplex formation. At low temp., the compd. adopts a stacked B-DNA type structure; destacking occurs on raising the temp. The sequence-dependent sugar ring geometry is present in this mol. The conformational parameters of d(T-A'-T-A') and d(T-A-T-A) are quite similar, thus substitution of dA by dA' has no measurable influence on the geometry of the sugar ring or on the backbone angles .beta., .gamma., and .delta..

L14 ANSWER 9 OF 11 CAPLUS COPYRIGHT 2000 ACS
AN 1982:558204 CAPLUS
DN 97:158204
TI The influence of the purine 2-amino group on DNA conformation and stability. Synthesis and conformational analysis of d[T(2-aminoA)]3
AU Gaffney, Barbara L.; Marky, Luis A.; Jones, Roger A.
CS Dep. Chem., Rutgers, State Univ. New Jersey, New Brunswick, NJ, 08903, USA
SO Nucleic Acids Res. (1982), 10(14), 4351-61
CODEN: NARHAD; ISSN: 0305-1048
DT Journal
LA English
AB A self-complementary hexanucleotide consisting of thymidine and **2-aminodeoxyadenosine**, d(TA')3, was synthesized by a solid phase phosphotriester method. Melting studies show that the addnl. H bond afforded by the 2-amino group substantially stabilizes the duplex. Moreover, conformational anal. using CD shows that a salt-induced conformational transition occurs, similar to the B.fwdarw.Z transition obsd. for d(CG)n oligonucleotides.

L14 ANSWER 10 OF 11 SCISEARCH COPYRIGHT 2000 ISI (R)
AN 80:500215 SCISEARCH
GA The Genuine Article (R) Number: KQ952
TI AMINOACYL DERIVATIVES OF NUCLEOSIDES, NUCLEOTIDES AND POLYNUCLEOTIDES .32.

SYNTHESIS OF AMINOACYLDINUCLEOSIDE PHOSPHATES DERIVED FROM 2'-AMINODEOXYADENOSINE AND 3'-AMINODEOXYADENOSINE

AU CHLADEK S (Reprint); BUTKE G
CS MICHIGAN CANC FDN, DETROIT, MI, 48201 (Reprint)
CYA USA
SO JOURNAL OF CARBOHYDRATES-NUCLEOSIDES-NUCLEOTIDES, (1980) Vol. 7, No. 5, pp. 297-313.
DT Article; Journal
FS LIFE
LA ENGLISH
REC Reference Count: 17

L14 ANSWER 11 OF 11 CAPLUS COPYRIGHT 2000 ACS
AN 1978:147689 CAPLUS
DN 88:147689
TI Analysis of the absorption spectrum of actinomycin D and the formation of its complexes with deoxynucleotides
AU Auer, Henry E.; Pawlowski-Konopnicki, Barbara E.; Chiao, Yu-Chih Chen; Krugh, Thomas R.
CS Dep. Biochem., Univ. Rochester Sch. Med., Rochester, N. Y., USA
SO Pept., Proc. Am. Pept. Symp., 5th (1977), 353-6. Editor(s): Goodman, Murray; Meienhofer, Johannes. Publisher: Wiley, New York, N. Y. CODEN: 37OBAT
DT Conference
LA English
AB Spectral anal. of actinomycin D (I) monomers, I dimers, and complexes between I and certain deoxynucleotides (2-aminodeoxyadenosine, dGMP, and dAMP) resolved the visible absorption spectrum of I into .gtoreq.3 unique electronic transitions. The 370 nm transition was identified with processes occurring preponderantly at the benzenoid binding site and the 490 nm transition with binding primarily at the quinoid site. The 440 nm transition apparently reflects significant contributions from both the benzenoid and quinoid portions of the phenoxazone drug.